

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Artavanis-Tsakonas, S. et al.

(ii) TITLE OF INVENTION: Therapeutic And Diagnostic Methods
And Compositions Based On Notch Proteins And
Nucleic Acids

7940X
(iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Pennie & Edmonds
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- (C) CITY: New York
- (D) STATE: New York
- (E) COUNTRY: U.S.A.
- (F) ZIP: 10036

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

B
(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/083,590
- (B) FILING DATE: 25-JUN-1993
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Misrock, S. Leslie
- (B) REGISTRATION NUMBER: 18,872
- (C) REFERENCE/DOCKET NUMBER: 7326-015

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 212 790-9090
- (B) TELEFAX: 212 8698864/9741
- (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2892 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 142..2640

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGAG GAATTATTCA AAACATAAAC ACAATAAACA ATTTGAGTAG TTGCCGCACA	60
CACACACACG CACAGCCCGT GGATTATTAC ACTAAAAGCG ACACTCAATC CAAAAAATCA	120
GCAACAAAAA CATCAATAAA C ATG CAT TGG ATT AAA TGT TTA TTA ACA GCA	171

																Met 1	His	Trp	Ile	Lys 5	Cys	Leu	Leu	Thr	Ala 10	
TTC	ATT	TGC	TTC	ACA	GTC	ATC	GTG	CAG	GTT	CAC	AGT	TCC	GGC	AGC	TTT						219					
Phe	Ile	Cys	Phe	Thr 15	Val	Ile	Val	Gln	Val 20	His	Ser	Ser	Gly	Ser 25	Phe											
GAG	TTG	CGC	CTG	AAG	TAC	TTC	AGC	AAC	GAT	CAC	GGG	CGG	GAC	AAC	GAG						267					
Glu	Leu	Arg	Leu 30	Lys	Tyr	Phe	Ser	Asn 35	Asp	His	Gly	Arg	Asp 40	Asn	Glu											
GGT	CGC	TGC	TGC	AGC	GGG	GAG	TCG	GAC	GGA	GCG	ACG	GGC	AAG	TGC	CTG						315					
Gly	Arg	Cys 45	Cys	Ser	Gly	Glu	Ser 50	Asp	Gly	Ala	Thr	Gly 55	Lys	Cys	Leu											
GGC	AGC	TGC	AAG	ACG	CGG	TTT	CGC	GTC	TGC	CTA	AAG	CAC	TAC	CAG	GCC						363					
Gly	Ser 60	Cys	Lys	Thr	Arg	Phe 65	Arg	Val	Cys	Leu	Lys 70	His	Tyr	Gln	Ala											
ACC	ATC	GAC	ACC	ACC	TCC	CAG	TGC	ACC	TAC	GGG	GAC	GTG	ATC	ACG	CCC						411					
Thr 75	Ile	Asp	Thr	Thr	Ser 80	Gln	Cys	Thr	Tyr	Gly 85	Asp	Val	Ile	Thr	Pro 90											
ATT	CTC	GGC	GAG	AAC	TCG	GTC	AAT	CTG	ACC	GAC	GCC	CAG	CGC	TTC	CAG						459					
Ile	Leu	Gly	Glu	Asn 95	Ser	Val	Asn	Leu	Thr 100	Asp	Ala	Gln	Arg	Phe 105	Gln											
AAC	AAG	GGC	TTC	ACG	AAT	CCC	ATC	CAG	TTC	CCC	TTC	TCG	TTC	TCA	TGG						507					
Asn	Lys	Gly	Phe 110	Thr	Asn	Pro	Ile	Gln 115	Phe	Pro	Phe	Ser	Phe 120	Ser	Trp											
CCG	GGT	ACC	TTC	TCG	CTG	ATC	GTC	GAG	GCC	TGG	CAT	GAT	ACG	AAC	AAT						555					
Pro	Gly	Thr 125	Phe	Ser	Leu	Ile	Val 130	Glu	Ala	Trp	His	Asp 135	Thr	Asn	Asn											
AGC	GGC	AAT	GCG	CGA	ACC	AAC	AAG	CTC	CTC	ATC	CAG	CGA	CTC	TTG	GTG						603					
Ser	Gly 140	Asn	Ala	Arg	Thr	Asn 145	Lys	Leu	Leu	Ile	Gln 150	Arg	Leu	Leu	Val											
CAG	CAG	GTA	CTG	GAG	GTG	TCC	TCC	GAA	TGG	AAG	ACG	AAC	AAG	TCG	GAA						651					
Gln 155	Gln	Val	Leu	Glu	Val 160	Ser	Ser	Glu	Trp	Lys 165	Thr	Asn	Lys	Ser	Glu 170											
TCG	CAG	TAC	ACG	TCG	CTG	GAG	TAC	GAT	TTC	CGT	GTC	ACC	TGC	GAT	CTC						699					
Ser	Gln	Tyr	Thr	Ser 175	Leu	Glu	Tyr	Asp	Phe 180	Arg	Val	Thr	Cys	Asp 185	Leu											
AAC	TAC	TAC	GGA	TCC	GGC	TGT	GCC	AAG	TTC	TGC	CGG	CCC	CGC	GAC	GAT						747					
Asn	Tyr	Tyr	Gly 190	Ser	Gly	Cys	Ala	Lys 195	Phe	Cys	Arg	Pro	Arg 200	Asp	Asp											
TCA	TTT	GGA	CAC	TCG	ACT	TGC	TCG	GAG	ACG	GGC	GAA	ATT	ATC	TGT	TTG						795					
Ser	Phe	Gly 205	His	Ser	Thr	Cys	Ser 210	Glu	Thr	Gly	Glu	Ile 215	Ile	Cys	Leu											
ACC	GGA	TGG	CAG	GGC	GAT	TAC	TGT	CAC	ATA	CCC	AAA	TGC	GCC	AAA	GGC						843					
Thr	Gly 220	Trp	Gln	Gly	Asp	Tyr 225	Cys	His	Ile	Pro	Lys 230	Cys	Ala	Lys	Gly											
TGT	GAA	CAT	GGA	CAT	TGC	GAC	AAA	CCC	AAT	CAA	TGC	GTT	TGC	CAA	CTG						891					
Cys 235	Glu	His	Gly	His	Cys 240	Asp	Lys	Pro	Asn	Gln 245	Cys	Val	Cys	Gln	Leu 250											
GGC	TGG	AAG	GGA	GCC	TTG	TGC	AAC	GAG	TGC	GTT	CTG	GAA	CCG	AAC	TGC						939					
Gly	Trp	Lys	Gly	Ala 255	Leu	Cys	Asn	Glu	Cys 260	Val	Leu	Glu	Pro	Asn 265	Cys											

ATC	CAT	GGC	ACC	TGC	AAC	AAA	CCC	TGG	ACT	TGC	ATC	TGC	AAC	GAG	GGT	987
Ile	His	Gly	Thr	Cys	Asn	Lys	Pro	Trp	Thr	Cys	Ile	Cys	Asn	Glu	Gly	
			270					275						280		
TGG	GGA	GGC	TTG	TAC	TGC	AAC	CAG	GAT	CTG	AAC	TAC	TGC	ACC	AAC	CAC	1035
Trp	Gly	Gly	Leu	Tyr	Cys	Asn	Gln	Asp	Leu	Asn	Tyr	Cys	Thr	Asn	His	
		285					290					295				
AGA	CCC	TGC	AAG	AAT	GGC	GGA	ACC	TGC	TTC	AAC	ACC	GGC	GAG	GGA	TTG	1083
Arg	Pro	Cys	Lys	Asn	Gly	Gly	Thr	Cys	Phe	Asn	Thr	Gly	Glu	Gly	Leu	
	300					305					310					
TAC	ACA	TGC	AAA	TGC	GCT	CCA	GGA	TAC	AGT	GGT	GAT	GAT	TGC	GAA	AAT	1131
Tyr	Thr	Cys	Lys	Cys	Ala	Pro	Gly	Tyr	Ser	Gly	Asp	Asp	Cys	Glu	Asn	
315					320					325					330	
GAG	ATC	TAC	TCC	TGC	GAT	GCC	GAT	GTC	AAT	CCC	TGC	CAG	AAT	GGT	GGT	1179
Glu	Ile	Tyr	Ser	Cys	Asp	Ala	Asp	Val	Asn	Pro	Cys	Gln	Asn	Gly	Gly	
				335				340						345		
ACC	TGC	ATC	GAT	GAG	CCG	CAC	ACA	AAA	ACC	GGC	TAC	AAG	TGT	CAT	TGC	1227
Thr	Cys	Ile	Asp	Glu	Pro	His	Thr	Lys	Thr	Gly	Tyr	Lys	Cys	His	Cys	
			350					355					360			
GCC	AAC	GGC	TGG	AGC	GGA	AAG	ATG	TGC	GAG	GAG	AAA	GTG	CTC	ACG	TGT	1275
Ala	Asn	Gly	Trp	Ser	Gly	Lys	Met	Cys	Glu	Glu	Lys	Val	Leu	Thr	Cys	
		365					370					375				
TCG	GAC	AAA	CCC	TGT	CAT	CAG	GGA	ATC	TGC	CGC	AAC	GTT	CGT	CCT	GGC	1323
Ser	Asp	Lys	Pro	Cys	His	Gln	Gly	Ile	Cys	Arg	Asn	Val	Arg	Pro	Gly	
	380					385					390					
TTG	GGA	AGC	AAG	GGT	CAG	GGC	TAC	CAG	TGC	GAA	TGT	CCC	ATT	GGC	TAC	1371
Leu	Gly	Ser	Lys	Gly	Gln	Gly	Tyr	Gln	Cys	Glu	Cys	Pro	Ile	Gly	Tyr	
395					400					405				410		
AGC	GGA	CCC	AAC	TGC	GAT	CTC	CAG	CTG	GAC	AAC	TGC	AGT	CCG	AAT	CCA	1419
Ser	Gly	Pro	Asn	Cys	Asp	Leu	Gln	Leu	Asp	Asn	Cys	Ser	Pro	Asn	Pro	
				415				420					425			
TGC	ATA	AAC	GGT	GGA	AGC	TGT	CAG	CCG	AGC	GGA	AAG	TGT	ATT	TGC	CCA	1467
Cys	Ile	Asn	Gly	Gly	Ser	Cys	Gln	Pro	Ser	Gly	Lys	Cys	Ile	Cys	Pro	
			430					435					440			
GCG	GGA	TTT	TCG	GGA	ACG	AGA	TGC	GAG	ACC	AAC	ATT	GAC	GAT	TGT	CTT	1515
Ala	Gly	Phe	Ser	Gly	Thr	Arg	Cys	Glu	Thr	Asn	Ile	Asp	Asp	Cys	Leu	
		445					450					455				
GGC	CAC	CAG	TGC	GAG	AAC	GGA	GGC	ACC	TGC	ATA	GAT	ATG	GTC	AAC	CAA	1563
Gly	His	Gln	Cys	Glu	Asn	Gly	Gly	Thr	Cys	Ile	Asp	Met	Val	Asn	Gln	
	460					465					470					
TAT	CGC	TGC	CAA	TGC	GTT	CCC	GGT	TTC	CAT	GGC	ACC	CAC	TGT	AGT	AGC	1611
Tyr	Arg	Cys	Gln	Cys	Val	Pro	Gly	Phe	His	Gly	Thr	His	Cys	Ser	Ser	
475					480					485					490	
AAA	GTT	GAC	TTG	TGC	CTC	ATC	AGA	CCG	TGT	GCC	AAT	GGA	GGA	ACC	TGC	1659
Lys	Val	Asp	Leu	Cys	Leu	Ile	Arg	Pro	Cys	Ala	Asn	Gly	Gly	Thr	Cys	
				495				500					505			
TTG	AAT	CTC	AAC	AAC	GAT	TAC	CAG	TGC	ACC	TGT	CGT	GCG	GGA	TTT	ACT	1707
Leu	Asn	Leu	Asn	Asn	Asp	Tyr	Gln	Cys	Thr	Cys	Arg	Ala	Gly	Phe	Thr	
			510					515					520			
GGC	AAG	GAT	TGC	TCT	GTG	GAC	ATC	GAT	GAG	TGC	AGC	AGT	GGA	CCC	TGT	1755
Gly	Lys	Asp	Cys	Ser	Val	Asp	Ile	Asp	Glu	Cys	Ser	Ser	Gly	Pro	Cys	
		525					530					535				

CAT His 540	AAC Asn 540	GGC Gly 540	GGC Gly 540	ACT Thr 540	TGC Cys 540	ATG Met 545	AAC Asn 545	CGC Arg 545	GTC Val 545	AAT Asn 550	TCG Ser 550	TTC Phe 550	GAA Glu 550	TGC Cys 550	GTG Val 550	1803
TGT Cys 555	GCC Ala 555	AAT Asn 555	GGT Gly 555	TTC Phe 555	AGG Arg 560	GGC Gly 560	AAG Lys 560	CAG Gln 560	TGC Cys 565	GAT Asp 565	GAG Glu 565	GAG Glu 565	TCC Ser 565	TAC Tyr 565	GAT Asp 570	1851
TCG Ser 575	GTG Val 575	ACC Thr 575	TTC Phe 575	GAT Asp 575	GCC Ala 575	CAC His 575	CAA Gln 575	TAT Tyr 575	GGA Gly 580	GCG Ala 580	ACC Thr 580	ACA Thr 580	CAA Gln 585	GCG Ala 585	AGA Arg 585	1899
GCC Ala 590	GAT Asp 590	GGT Gly 590	TTG Leu 590	ACC Thr 590	AAT Asn 590	GCC Ala 590	CAG Gln 595	GTA Val 595	GTC Val 595	CTA Leu 595	ATT Ile 595	GCT Ala 595	GTT Val 600	TTC Phe 600	TCC Ser 600	1947
GTT Val 605	GCG Ala 605	ATG Met 605	CCT Pro 605	TTG Leu 605	GTG Val 605	GCG Ala 610	GTT Val 610	ATT Ile 610	GCG Ala 610	GCG Ala 610	TGC Cys 615	GTG Val 615	GTC Val 615	TTC Phe 615	TGC Cys 615	1995
ATG Met 620	AAG Lys 620	CGC Arg 620	AAG Lys 620	CGT Arg 620	AAG Lys 620	CGT Arg 625	GCT Ala 625	CAG Gln 625	GAA Glu 625	AAG Lys 625	GAC Asp 630	GAC Asp 630	GCG Ala 630	GAG Glu 630	GCC Ala 630	2043
AGG Arg 635	AAG Lys 635	CAG Gln 635	AAC Asn 635	GAA Glu 635	CAG Gln 640	AAT Asn 640	GCG Ala 640	GTG Val 640	GCC Ala 640	ACA Thr 645	ATG Met 645	CAT His 645	CAC His 645	AAT Asn 645	GGC Gly 650	2091
AGT Ser 655	GGG Gly 655	GTG Val 655	GGT Gly 655	GTA Val 655	GCT Ala 655	TTG Leu 655	GCT Ala 655	TCA Ser 655	GCC Ala 660	TCT Ser 660	CTG Leu 660	GGC Gly 660	GGC Gly 660	AAA Lys 665	ACT Thr 665	2139
GGC Gly 670	AGC Ser 670	AAC Asn 670	AGC Ser 670	GGT Gly 670	CTC Leu 670	ACC Thr 670	TTC Phe 670	GAT Asp 675	GGC Gly 675	GGC Gly 675	AAC Asn 675	CCG Pro 675	AAT Asn 680	ATC Ile 680	ATC Ile 680	2187
AAA Lys 685	AAC Asn 685	ACC Thr 685	TGG Trp 685	GAC Asp 685	AAG Lys 685	TCG Ser 690	GTC Val 690	AAC Asn 690	AAC Asn 690	ATT Ile 690	TGT Cys 695	GCC Ala 695	TCA Ser 695	GCA Ala 695	GCA Ala 695	2235
GCA Ala 700	GCG Ala 700	GCG Ala 700	GCG Ala 700	GCG Ala 700	GCA Ala 705	GCA Ala 705	GCG Ala 705	GCG Ala 705	GAC Asp 705	GAG Glu 710	TGT Cys 710	CTC Leu 710	ATG Met 710	TAC Tyr 710	GGC Gly 710	2283
GGA Gly 715	TAT Tyr 715	GTG Val 715	GCC Ala 715	TCG Ser 720	GTG Val 720	GCG Ala 720	GAT Asp 720	AAC Asn 725	AAC Asn 725	AAT Asn 725	GCC Ala 725	AAC Asn 725	TCA Ser 730	GAC Asp 730	TTT Phe 730	2331
TGT Cys 735	GTG Val 735	GCT Ala 735	CCG Pro 735	CTA Leu 735	CAA Gln 735	AGA Arg 735	GCC Ala 735	AAG Lys 735	TCG Ser 740	CAA Gln 740	AAG Lys 740	CAA Gln 740	CTC Leu 745	AAC Asn 745	ACC Thr 745	2379
GAT Asp 750	CCC Pro 750	ACG Thr 750	CTC Leu 750	ATG Met 750	CAC His 750	CGC Arg 750	GGT Gly 755	TCG Ser 755	CCG Pro 755	GCA Ala 755	GGC Gly 755	AGC Ser 760	TCA Ser 760	GCC Ala 760	AAG Lys 760	2427
GGA Gly 765	GCG Ala 765	TCT Ser 765	GGC Gly 765	GGA Gly 765	GGA Gly 765	CCG Pro 770	GGA Gly 770	GCG Ala 770	GCG Ala 770	GAG Glu 775	GGC Gly 775	AAG Lys 775	AGG Arg 775	ATC Ile 775	TCT Ser 775	2475
GTT Val 780	TTA Leu 780	GGC Gly 780	GAG Glu 780	GGT Gly 780	TCC Ser 785	TAC Tyr 785	TGT Cys 785	AGC Ser 785	CAG Gln 785	CGT Arg 790	TGG Trp 790	CCC Pro 790	TCG Ser 790	TTG Leu 790	GCG Ala 790	2523
GCG Ala 795	GCG Ala 795	GGA Gly 795	GTG Val 795	GCC Ala 795	GGA Gly 800	GCC Ala 795	TGT Cys 795	TCA Ser 795	TCC Ser 795	CAG Gln 805	CTA Leu 805	ATG Met 805	GCT Ala 805	GCA Ala 805	GCT Ala 810	2571

TCG GCA GCG GGC AGC GGA GCG GGG ACG GCG CAA CAG CAG CGA TCC GTG	2619
Ser Ala Ala Gly Ser Gly Ala Gly Thr Ala Gln Gln Gln Arg Ser Val	
815 820 825	
GTC TGC GGC ACT CCG CAT ATG TAACTCCAAA AATCCGGAAG GGCTCCTGGT	2670
Val Cys Gly Thr Pro His Met	
830	
AAATCCGGAG AAATCCGCAT GGAGGAGCTG ACAGCACATA CACAAAGAAA AGACTGGGTT	2730
GGGTTCAAAA TGTGAGAGAG ACGCCAAAAT GTTGTGTGTG ATTGAAGCAG TTTAGTCGTC	2790
ACGAAAAATG AAAAATCTGT AACAGGCATA ACTCGTAAAC TCCCTAAAAA ATTTGTATAG	2850
TAATTAGCAA AGCTGTGACC CAGCCGTTTC GATCCCGAAT TC	2892

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

B

Met	His	Trp	Ile	Lys	Cys	Leu	Leu	Thr	Ala	Phe	Ile	Cys	Phe	Thr	Val
1				5					10					15	
Ile	Val	Gln	Val	His	Ser	Ser	Gly	Ser	Phe	Glu	Leu	Arg	Leu	Lys	Tyr
			20					25					30		
Phe	Ser	Asn	Asp	His	Gly	Arg	Asp	Asn	Glu	Gly	Arg	Cys	Cys	Ser	Gly
		35					40					45			
Glu	Ser	Asp	Gly	Ala	Thr	Gly	Lys	Cys	Leu	Gly	Ser	Cys	Lys	Thr	Arg
	50					55					60				
Phe	Arg	Val	Cys	Leu	Lys	His	Tyr	Gln	Ala	Thr	Ile	Asp	Thr	Thr	Ser
65					70					75					80
Gln	Cys	Thr	Tyr	Gly	Asp	Val	Ile	Thr	Pro	Ile	Leu	Gly	Glu	Asn	Ser
				85					90					95	
Val	Asn	Leu	Thr	Asp	Ala	Gln	Arg	Phe	Gln	Asn	Lys	Gly	Phe	Thr	Asn
			100					105					110		
Pro	Ile	Gln	Phe	Pro	Phe	Ser	Phe	Ser	Trp	Pro	Gly	Thr	Phe	Ser	Leu
		115					120					125			
Ile	Val	Glu	Ala	Trp	His	Asp	Thr	Asn	Asn	Ser	Gly	Asn	Ala	Arg	Thr
	130					135					140				
Asn	Lys	Leu	Leu	Ile	Gln	Arg	Leu	Leu	Val	Gln	Gln	Val	Leu	Glu	Val
145					150					155					160
Ser	Ser	Glu	Trp	Lys	Thr	Asn	Lys	Ser	Glu	Ser	Gln	Tyr	Thr	Ser	Leu
				165					170					175	
Glu	Tyr	Asp	Phe	Arg	Val	Thr	Cys	Asp	Leu	Asn	Tyr	Tyr	Gly	Ser	Gly
			180					185					190		
Cys	Ala	Lys	Phe	Cys	Arg	Pro	Arg	Asp	Asp	Ser	Phe	Gly	His	Ser	Thr
		195					200					205			

Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu Thr Gly Trp Gln Gly Asp
 210 215 220
 Tyr Cys His Ile Pro Lys Cys Ala Lys Gly Cys Glu His Gly His Cys
 225 230 235 240
 Asp Lys Pro Asn Gln Cys Val Cys Gln Leu Gly Trp Lys Gly Ala Leu
 245 250 255
 Cys Asn Glu Cys Val Leu Glu Pro Asn Cys Ile His Gly Thr Cys Asn
 260 265 270
 Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly Trp Gly Gly Leu Tyr Cys
 275 280 285
 Asn Gln Asp Leu Asn Tyr Cys Thr Asn His Arg Pro Cys Lys Asn Gly
 290 295 300
 Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu Tyr Thr Cys Lys Cys Ala
 305 310 315 320
 Pro Gly Tyr Ser Gly Asp Asp Cys Glu Asn Glu Ile Tyr Ser Cys Asp
 325 330 335
 Ala Asp Val Asn Pro Cys Gln Asn Gly Gly Thr Cys Ile Asp Glu Pro
 340 345 350
 His Thr Lys Thr Gly Tyr Lys Cys His Cys Ala Asn Gly Trp Ser Gly
 355 360 365
 Lys Met Cys Glu Glu Lys Val Leu Thr Cys Ser Asp Lys Pro Cys His
 370 375 380
 Gln Gly Ile Cys Arg Asn Val Arg Pro Gly Leu Gly Ser Lys Gly Gln
 385 390 395 400
 Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr Ser Gly Pro Asn Cys Asp
 405 410 415
 Leu Gln Leu Asp Asn Cys Ser Pro Asn Pro Cys Ile Asn Gly Gly Ser
 420 425 430
 Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro Ala Gly Phe Ser Gly Thr
 435 440 445
 Arg Cys Glu Thr Asn Ile Asp Asp Cys Leu Gly His Gln Cys Glu Asn
 450 455 460
 Gly Gly Thr Cys Ile Asp Met Val Asn Gln Tyr Arg Cys Gln Cys Val
 465 470 475 480
 Pro Gly Phe His Gly Thr His Cys Ser Ser Lys Val Asp Leu Cys Leu
 485 490 495
 Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys Leu Asn Leu Asn Asn Asp
 500 505 510
 Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr Gly Lys Asp Cys Ser Val
 515 520 525
 Asp Ile Asp Glu Cys Ser Ser Gly Pro Cys His Asn Gly Gly Thr Cys
 530 535 540
 Met Asn Arg Val Asn Ser Phe Glu Cys Val Cys Ala Asn Gly Phe Arg
 545 550 555 560
 Gly Lys Gln Cys Asp Glu Glu Ser Tyr Asp Ser Val Thr Phe Asp Ala

B

99

565								570								575							
His	Gln	Tyr	Gly	Ala	Thr	Thr	Gln	Ala	Arg	Ala	Asp	Gly	Leu	Thr	Asn								
			580					585					590										
Ala	Gln	Val	Val	Leu	Ile	Ala	Val	Phe	Ser	Val	Ala	Met	Pro	Leu	Val								
		595					600					605											
Ala	Val	Ile	Ala	Ala	Cys	Val	Val	Phe	Cys	Met	Lys	Arg	Lys	Arg	Lys								
	610					615					620												
Arg	Ala	Gln	Glu	Lys	Asp	Asp	Ala	Glu	Ala	Arg	Lys	Gln	Asn	Glu	Gln								
	625				630				635					640									
Asn	Ala	Val	Ala	Thr	Met	His	His	Asn	Gly	Ser	Gly	Val	Gly	Val	Ala								
				645					650					655									
Leu	Ala	Ser	Ala	Ser	Leu	Gly	Gly	Lys	Thr	Gly	Ser	Asn	Ser	Gly	Leu								
			660						665					670									
Thr	Phe	Asp	Gly	Gly	Asn	Pro	Asn	Ile	Ile	Lys	Asn	Thr	Trp	Asp	Lys								
		675					680					685											
Ser	Val	Asn	Asn	Ile	Cys	Ala	Ser	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala								
	690					695					700												
Ala	Ala	Ala	Asp	Glu	Cys	Leu	Met	Tyr	Gly	Gly	Tyr	Val	Ala	Ser	Val								
	705				710				715					720									
Ala	Asp	Asn	Asn	Asn	Ala	Asn	Ser	Asp	Phe	Cys	Val	Ala	Pro	Leu	Gln								
				725					730					735									
Arg	Ala	Lys	Ser	Gln	Lys	Gln	Leu	Asn	Thr	Asp	Pro	Thr	Leu	Met	His								
			740						745					750									
Arg	Gly	Ser	Pro	Ala	Gly	Ser	Ser	Ala	Lys	Gly	Ala	Ser	Gly	Gly	Gly								
		755					760					765											
Pro	Gly	Ala	Ala	Glu	Gly	Lys	Arg	Ile	Ser	Val	Leu	Gly	Glu	Gly	Ser								
	770					775					780												
Tyr	Cys	Ser	Gln	Arg	Trp	Pro	Ser	Leu	Ala	Ala	Ala	Gly	Val	Ala	Gly								
	785				790				795					800									
Ala	Cys	Ser	Ser	Gln	Leu	Met	Ala	Ala	Ala	Ser	Ala	Ala	Gly	Ser	Gly								
				805					810					815									
Ala	Gly	Thr	Ala	Gln	Gln	Gln	Arg	Ser	Val	Val	Cys	Gly	Thr	Pro	His								
			820				825						830										

Met

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 442..1320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGAGTCGAG CGCCGTGCTT CGAGCGGTGA TGAGCCCCTT TTCTGTCAAC GCTAAAGATC	60
TACAAAACAT CAGCGCCTAT CAAGTGGAAG TGTCAAGTGT GAACAAAACA AAAACGAGAG	120
AAGCACATAC TAAGGTCCAT ATAAATAATA AATAATAATT GTGTGTGATA ACAACATTAT	180
CCAAACAAAA CCAAACAAAA CGAAGGCAAA GTGGAGAAAA TGATACAGCA TCCAGAGTAC	240
GGCCGTTATT CAGCTATCCA GAGCAAGTGT AGTGTGGCAA AATAGAAACA AACAAAGGCA	300
CCAAAATCTG CATACTGGG CTAATTAAGG CTGCCCAGCG AATTACATT TGTGTGGTGC	360
CAATCCAGAG TGAATCCGAA ACAAACTCCA TCTAGATCGC CAACCAGCAT CACGCTCGCA	420
AACGCCCCCA GAATGTACAA A ATG TTT AGG AAA CAT TTT CGG CGA AAA CCA	471
Met Phe Arg Lys His Phe Arg Arg Lys Pro	
1 5 10	
GCT ACG TCG TCG TCG TTG GAG TCA ACA ATA GAA TCA GCA GAC AGC CTG	519
Ala Thr Ser Ser Ser Leu Glu Ser Thr Ile Glu Ser Ala Asp Ser Leu	
15 20 25	
GGA ATG TCC AAG AAG ACG GCG ACA AAA AGG CAG CGT CCG AGG CAT CGG	567
Gly Met Ser Lys Lys Thr Ala Thr Lys Arg Gln Arg Pro Arg His Arg	
30 35 40	
GTA CCC AAA ATC GCG ACC CTG CCA TCG ACG ATC CGC GAT TGT CGA TCA	615
Val Pro Lys Ile Ala Thr Leu Pro Ser Thr Ile Arg Asp Cys Arg Ser	
45 50 55	
TTA AAG TCT GCC TGC AAC TTA ATT GCT TTA ATT TTA ATA CTG TTA GTC	663
Leu Lys Ser Ala Cys Asn Leu Ile Ala Leu Ile Leu Ile Leu Leu Val	
60 65 70	
CAT AAG ATA TCC GCA GCT GGT AAC TTC GAG CTG GAA ATA TTA GAA ATC	711
His Lys Ile Ser Ala Ala Gly Asn Phe Glu Leu Glu Ile Leu Glu Ile	
75 80 85 90	
TCA AAT ACC AAC AGC CAT CTA CTC AAC GGC TAT TGC TGC GGC ATG CCA	759
Ser Asn Thr Asn Ser His Leu Leu Asn Gly Tyr Cys Cys Gly Met Pro	
95 100 105	
GCG GAA CTT AGG GCC ACC AAG ACG ATA GGC TGC TCG CCA TGC ACG ACG	807
Ala Glu Leu Arg Ala Thr Lys Thr Ile Gly Cys Ser Pro Cys Thr Thr	
110 115 120	
GCA TTC CGG CTG TGC CTG AAG GAG TAC CAG ACC ACG GAG CAG GGT GCC	855
Ala Phe Arg Leu Cys Leu Lys Glu Tyr Gln Thr Thr Glu Gln Gly Ala	
125 130 135	
AGC ATA TCC ACG GGC TGT TCG TTT GGC AAC GCC ACC ACC AAG ATA CTG	903
Ser Ile Ser Thr Gly Cys Ser Phe Gly Asn Ala Thr Thr Lys Ile Leu	
140 145 150	
GGT GGC TCC AGC TTT GTG CTC AGC GAT CCG GGT GTG GGA GCC ATT GTG	951
Gly Gly Ser Ser Phe Val Leu Ser Asp Pro Gly Val Gly Ala Ile Val	
155 160 165 170	
CTG CCC TTT ACG TTT CGT TGG ACG AAG TCG TTT ACG CTG ATA CTG CAG	999
Leu Pro Phe Thr Phe Arg Trp Thr Lys Ser Phe Thr Leu Ile Leu Gln	
175 180 185	
GCG TTG GAT ATG TAC AAC ACA TCC TAT CCA GAT GCG GAG AGG TTA ATT	1047

Ala	Leu	Asp	Met	Tyr	Asn	Thr	Ser	Tyr	Pro	Asp	Ala	Glu	Arg	Leu	Ile		
			190					195					200				
GAG	GAA	ACA	TCA	TAC	TCG	GGC	GTG	ATA	CTG	CCG	TCG	CCG	GAG	TGG	AAG		1095
Glu	Glu	Thr	Ser	Tyr	Ser	Gly	Val	Ile	Leu	Pro	Ser	Pro	Glu	Trp	Lys		
		205					210					215					
ACG	CTG	GAC	CAC	ATC	GGG	CGG	AAC	GCG	CGG	ATC	ACC	TAC	CGT	GTC	CGG		1143
Thr	Leu	Asp	His	Ile	Gly	Arg	Asn	Ala	Arg	Ile	Thr	Tyr	Arg	Val	Arg		
	220					225					230						
GTG	CAA	TGC	GCC	GTT	ACC	TAC	TAC	AAC	ACG	ACC	TGC	ACG	ACC	TTC	TGC		1191
Val	Gln	Cys	Ala	Val	Thr	Tyr	Tyr	Asn	Thr	Thr	Cys	Thr	Thr	Phe	Cys		
235					240				245						250		
CGT	CCG	CGG	GAC	GAT	CAG	TTC	GGT	CAC	TAC	GCC	TGC	GGC	TCC	GAG	GGT		1239
Arg	Pro	Arg	Asp	Asp	Gln	Phe	Gly	His	Tyr	Ala	Cys	Gly	Ser	Glu	Gly		
				255					260					265			
CAG	AAG	CTC	TGC	CTG	AAT	GGC	TGG	CAG	GGC	GTC	AAC	TGC	GAG	GAG	GCC		1287
Gln	Lys	Leu	Cys	Leu	Asn	Gly	Trp	Gln	Gly	Val	Asn	Cys	Glu	Glu	Ala		
			270					275					280				
ATA	TGC	AAG	GCG	GGC	TGC	GAC	CCC	GTC	CAC	GGC							1320
Ile	Cys	Lys	Ala	Gly	Cys	Asp	Pro	Val	His	Gly							
		285					290										

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Phe	Arg	Lys	His	Phe	Arg	Arg	Lys	Pro	Ala	Thr	Ser	Ser	Ser	Leu		
1				5					10					15			
Glu	Ser	Thr	Ile	Glu	Ser	Ala	Asp	Ser	Leu	Gly	Met	Ser	Lys	Lys	Thr		
			20					25					30				
Ala	Thr	Lys	Arg	Gln	Arg	Pro	Arg	His	Arg	Val	Pro	Lys	Ile	Ala	Thr		
		35					40					45					
Leu	Pro	Ser	Thr	Ile	Arg	Asp	Cys	Arg	Ser	Leu	Lys	Ser	Ala	Cys	Asn		
	50					55					60						
Leu	Ile	Ala	Leu	Ile	Leu	Ile	Leu	Leu	Val	His	Lys	Ile	Ser	Ala	Ala		
65				70					75						80		
Gly	Asn	Phe	Glu	Leu	Glu	Ile	Leu	Glu	Ile	Ser	Asn	Thr	Asn	Ser	His		
			85					90					95				
Leu	Leu	Asn	Gly	Tyr	Cys	Cys	Gly	Met	Pro	Ala	Glu	Leu	Arg	Ala	Thr		
		100					105						110				
Lys	Thr	Ile	Gly	Cys	Ser	Pro	Cys	Thr	Thr	Ala	Phe	Arg	Leu	Cys	Leu		
		115					120					125					
Lys	Glu	Tyr	Gln	Thr	Thr	Glu	Gln	Gly	Ala	Ser	Ile	Ser	Thr	Gly	Cys		
	130					135					140						
Ser	Phe	Gly	Asn	Ala	Thr	Thr	Lys	Ile	Leu	Gly	Gly	Ser	Ser	Phe	Val		

145		150		155		160
Leu Ser Asp Pro Gly Val Gly Ala Ile Val Leu Pro Phe Thr Phe Arg	165		170		175	
Trp Thr Lys Ser Phe Thr Leu Ile Leu Gln Ala Leu Asp Met Tyr Asn	180		185		190	
Thr Ser Tyr Pro Asp Ala Glu Arg Leu Ile Glu Glu Thr Ser Tyr Ser	195		200		205	
Gly Val Ile Leu Pro Ser Pro Glu Trp Lys Thr Leu Asp His Ile Gly	210		215		220	
Arg Asn Ala Arg Ile Thr Tyr Arg Val Arg Val Gln Cys Ala Val Thr	225		230		235	240
Tyr Tyr Asn Thr Thr Cys Thr Thr Phe Cys Arg Pro Arg Asp Asp Gln	245		250		255	
Phe Gly His Tyr Ala Cys Gly Ser Glu Gly Gln Lys Leu Cys Leu Asn	260		265		270	
Gly Trp Gln Gly Val Asn Cys Glu Glu Ala Ile Cys Lys Ala Gly Cys	275		280		285	
Asp Pro Val His Gly	290					

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGTGGACTT CCTTCGTGTA TTGGTGGGAG CCCTCGGGAA CGGGGGGTAA CACTGAAAGG	60
TCGAGTACCC ATTTCCGTCA TAACGGGTTG GTCGCCCCCT AGGGGTCGGA GTCAGGTGGA	120
CGGGAGGTCTG ACAACGCCCCG GGGGACGGGT GGTACATGGT GTAAGGTCTT TACCGGACCG	180
GGCAAACGGG TCACACCGAA AGGGGTGAAC GGTAAC TACG GGGTCGTCCT GCCCGTCCAT	240
CGAGTCTGGT AAGAGGGTCG CCTTAAG	267

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCCTTC CATTATACGT GACTTTTCTG AAAGTGTAGC CACCCTAGTG TCTCTAACTC	60
CCTCTGGAGT TTGTCAGCTT TGGTCTTTTC AAAGAGCAGG CTCTCTTCAA GCTCCTTAAT	120
GCGGGCATGC TCCAGTTTGG TCTGCGTCTC AAGATCACCT TTGGTAATTG ATTCTTCTTC	180
AACCCGGAAC TGAAGGCTGG CTCTCACCTT CTAGGCAGAG CAGGAATTCC GAGGTGGATG	240
TGTTAGATGT GAATGTCCGT GGCCCAGATG GCTGCACCCC ATTGATGTTG GCTTCTCTCC	300
GAGGAGGCAG CTCAGATTTG AGTGATGAAG ATGAAGATGC AGAGGACTGT TCTGCTAACA	360
TCATCACAGA CTTGGTCTAC CAGGGTGCCA GCCTCCAGNC CAGACAGACC GGACTGGTGA	420
GATGGCCCTG CACCTTGCAG CCCGCTACTC ACGGGCTGAT GCTGCCAAGC GTCTCCTGGA	480
TGCAGGTGCA GATGCCAATG CCCAGGACAA CATGGGCCGC TGTCCACTCC ATGCTGCAGT	540
GGCACGTGAT GCCAAGGTGT ATTCAGATCT GTTA	574

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

B
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCCAGATTCT GATTCGCAAC CGAGTAACTG ATCTAGATGC CAGGATGAAT GATGGTACTA	60
CACCCCTGAT CCTGGCTGCC CGCCTGGCTG TGGAGGGAAT GGTGGCAGAA CTGATCAACT	120
GCCAAGCGGA TGTGAATGCA GTGGATGACC ATGGAAAATC TGCTCTTCAC TGGGCAGCTG	180
CTGTCAATAA TGTGGAGGCA ACTCTTTTGT TGTTGAAAAA TGGGGCCAAC CGAGACATGC	240
AGGACAACAA GGAAGAGACA CCTCTGTTTC TTGCTGCCCCG GGAGGAGCTA TAAGC	295

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCATT CAGGAGGAAA GGGTGGGGAG AGAAGCAGGC ACCCACTTTC CCGTGGCTGG	60
ACTCGTTCCC AGGTGGCTCC ACCGGCAGCT GTGACCGCCG CAGGTGGGGG CGGAGTGCCA	120
TTCAGAAAAT TCCAGAAAAG CCCTACCCCA ACTCGGACGG CAACGTCACA CCCGTGGGTA	180

GCAACTGGCA CACAAACAGC CAGCGTGTCT GGGGCACGGG GGGATGGCAC CCCCTGCAGG 240
CAGAGCTG 248

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TACGTATCTC GAGCACAGAC AGCTGACGTA CACTTTTNNNA GTGCGAGGGA CATTCGTCCG 60
ACCAGTACGA ACATTTAGGC TCAGTACGGT AGGTCCATGG CCAAGACTAG GAGACGTAGG 120
GAGCTACAGG TCCCGCTCGC TAAACTCGGA CCACTGAAAC CTCCGGTCGA CAGTCGGTAA 180
GCGAACAAGA GGGCCAGATC TTAGAGAAGG TGTCGCGGCG AGACTCGGGC TCGGGTCAGG 240
CGGCCTTAAG GACGTCGGGC CCNNNAGGTG ATCAAGATCT CGNCNCGGCG GGCGCCACCT 300
CGAGGNCGAA AACAAGGGAA ATC 323

B
(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..3234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGC CAG GAG GAC GCG GGC AAC AAG GTC TGC AGC CTG CAG TGC AAC AAC 48
Cys Gln Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn
1 5 10 15
CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC 96
His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp
20 25 30
CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGG AAG TAC TTC AGT 144
Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser
35 40 45
GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC 192
Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp
50 55 60
GGC TTT GAC TGC CAG CGT GCG GAA GGC CAG TGC AAC CCC CTG TAC GAC 240

Gly 65	Phe	Asp	Cys	Gln	Arg 70	Ala	Glu	Gly	Gln	Cys 75	Asn	Pro	Leu	Tyr	Asp 80	
CAG Gln	TAC Tyr	TGC Cys	AAG Lys	GAC Asp 85	CAC His	TTC Phe	AGC Ser	GAC Asp	GGG Gly 90	CAC His	TGC Cys	GAC Asp	CAG Gln	GGC Gly 95	TGC Cys	288
AAC Asn	AGC Ser	GCG Ala	GAG Glu 100	TGC Cys	GAG Glu	TGG Trp	GAC Asp	GGG Gly 105	CTG Leu	GAC Asp	TGT Cys	GCG Ala	GAG Glu 110	CAT His	GTA Val	336
CCC Pro	GAG Glu	AGG Arg 115	CTG Leu	GCG Ala	GCC Ala	GGC Gly	ACG Thr 120	CTG Leu	GTG Val	GTG Val	GTG Val	GTG Val	CTG Leu	ATG Met	CCG Pro	384
CCG Pro	GAG Glu 130	CAG Gln	CTG Leu	CGC Arg	AAC Asn	AGC Ser 135	TCC Ser	TTC Phe	CAC His	TTC Phe	CTG Leu 140	CGG Arg	GAG Glu	CTC Leu	AGC Ser	432
CGC Arg 145	GTG Val	CTG Leu	CAC His	ACC Thr	AAC Asn 150	GTG Val	GTC Val	TTC Phe	AAG Lys	CGT Arg 155	GAC Asp	GCA Ala	CAC His	GGC Gly	CAG Gln 160	480
CAG Gln	ATG Met	ATC Ile	TTC Phe	CCC Pro 165	TAC Tyr	TAC Tyr	GGC Gly	CGC Arg	GAG Glu 170	GAG Glu	GAG Glu	CTG Leu	CGC Arg	AAG Lys 175	CAC His	528
CCC Pro	ATC Ile	AAG Lys	CGT Arg 180	GCC Ala	GCC Ala	GAG Glu	GGC Gly	TGG Trp 185	GCC Ala	GCA Ala	CCT Pro	GAC Asp	GCC Ala 190	CTG Leu	CTG Leu	576
GGC Gly	CAG Gln	GTG Val 195	AAG Lys	GCC Ala	TCG Ser	CTG Leu	CTC Leu 200	CCT Pro	GGT Gly	GGC Gly	AGC Ser	GAG Glu 205	GGT Gly	GGG Gly	CGG Arg	624
CGG Arg 210	CGG Arg	AGG Arg	GAG Glu	CTG Leu	GAC Asp	CCC Pro 215	ATG Met	GAC Asp	GTC Val	CGC Arg	GGC Gly 220	TCC Ser	ATC Ile	GTC Val	TAC Tyr	672
CTG Leu 225	GAG Glu	ATT Ile	GAC Asp	AAC Asn	CGG Arg 230	CAG Gln	TGT Cys	GTG Val	CAG Gln	GCC Ala 235	TCC Ser	TCG Ser	CAG Gln	TGC Cys	TTC Phe 240	720
CAG Gln	AGT Ser	GCC Ala	ACC Thr	GAC Asp 245	GTG Val	GCC Ala	GCA Ala	TTC Phe	CTG Leu 250	GGA Gly	GCG Ala	CTC Leu	GCC Ala	TCG Ser 255	CTG Leu	768
GGC Gly	AGC Ser	CTC Leu	AAC Asn 260	ATC Ile	CCC Pro	TAC Tyr	AAG Lys	ATC Ile 265	GAG Glu	GCC Ala	GTG Val	CAG Gln	AGT Ser 270	GAG Glu	ACC Thr	816
GTG Val	GAG Glu	CCG Pro 275	CCC Pro	CCG Pro	CCG Pro	GCG Ala	CAG Gln 280	CTG Leu	CAC His	TTC Phe	ATG Met	TAC Tyr 285	GTG Val	GCG Ala	GCG Ala	864
GCC Ala 290	GCC Ala	TTT Phe	GTG Val	CTT Leu	CTG Leu	TTC Phe 295	TTC Phe	GTG Val	GGC Gly	TGC Cys	GGG Gly 300	GTG Val	CTG Leu	CTG Leu	TCC Ser	912
CGC Arg 305	AAG Lys	CGC Arg	CGG Arg	CGG Arg	CAG Gln 310	CAT His	GGC Gly	CAG Gln	CTC Leu	TGG Trp 315	TTC Phe	CCT Pro	GAG Glu	GGC Gly	TTC Phe 320	960
AAA Lys	GTG Val	TCT Ser	GAG Glu	GCC Ala 325	AGC Ser	AAG Lys	AAG Lys	AAG Lys	CGG Arg 330	CGG Arg	GAG Glu	CCC Pro	CTC Leu	GGC Gly 335	GAG Glu	1008

B

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GAC Asp	TCC Ser	GTG Val	GGC Gly 340	CTC Leu	AAG Lys	CCC Pro	CTG Leu	AAG Lys 345	AAC Asn	GCT Ala	TCA Ser	GAC Asp	GGT Gly 350	GCC Ala	CTC Leu	1056
ATG Met	GAC Asp	GAC Asp 355	AAC Asn	CAG Gln	AAT Asn	GAG Glu	TGG Trp 360	GGG Gly	GAC Asp	GAG Glu	GAC Asp	CTG Leu 365	GAG Glu	ACC Thr	AAG Lys	1104
AAG Lys	TTC Phe 370	CGG Arg	TTC Phe	GAG Glu	GAG Glu	CCC Pro 375	GTG Val	GTT Val	CTG Leu	CCT Pro	GAC Asp 380	CTG Leu	GAC Asp	GAC Asp	CAG Gln	1152
ACA Thr 385	GAC Asp	CAC His	CGG Arg	CAG Gln	TGG Trp 390	ACT Thr	CAG Gln	CAG Gln	CAC His	CTG Leu 395	GAT Asp	GCC Ala	GCT Ala	GAC Asp	CTG Leu 400	1200
CGC Arg	ATG Met	TCT Ser	GCC Ala	ATG Met 405	GCC Ala	CCC Pro	ACA Thr	CCG Pro	CCC Pro 410	CAG Gln	GGT Gly	GAG Glu	GTT Val	GAC Asp 415	GCC Ala	1248
GAC Asp	TGC Cys	ATG Met	GAC Asp 420	GTC Val	AAT Asn	GTC Val	CGC Arg	GGG Gly 425	CCT Pro	GAT Asp	GGC Gly	TTC Phe	ACC Thr 430	CCG Pro	CTC Leu	1296
ATG Met	ATC Ile	GCC Ala 435	TCC Ser	TGC Cys	AGC Ser	GGG Gly	GGC Gly 440	GGC Gly	CTG Leu	GAG Glu	ACG Thr	GGC Gly 445	AAC Asn	AGC Ser	GAG Glu	1344
GAA Glu	GAG Glu 450	GAG Glu	GAC Asp	GCG Ala	CCG Pro	GCC Ala 455	GTC Val	ATC Ile	TCC Ser	GAC Asp	TTC Phe 460	ATC Ile	TAC Tyr	CAG Gln	GGC Gly	1392
GCC Ala 465	AGC Ser	CTG Leu	CAC His	AAC Asn	CAG Gln 470	ACA Thr	GAC Asp	CGC Arg	ACG Thr	GGC Gly 475	GAG Glu	ACC Thr	GCC Ala	TTG Leu	CAC His 480	1440
CTG Leu	GCC Ala	GCC Ala	CGC Arg	TAC Tyr 485	TCA Ser	CGC Arg	TCT Ser	GAT Asp	GCC Ala 490	GCC Ala	AAG Lys	CGC Arg	CTG Leu 495	CTG Leu	GAG Glu	1488
GCC Ala	AGC Ser	GCA Ala	GAT Asp 500	GCC Ala	AAC Asn	ATC Ile	CAG Gln	GAC Asp 505	AAC Asn	ATG Met	GGC Gly	CGC Arg	ACC Thr 510	CCG Pro	CTG Leu	1536
CAT His	GCG Ala	GCT Ala 515	GTG Val	TCT Ser	GCC Ala	GAC Asp	GCA Ala 520	CAA Gln	GGT Gly	GTC Val	TTC Phe	CAG Gln 525	ATC Ile	CTG Leu	ATC Ile	1584
CGG Arg	AAC Asn 530	CGA Arg	GCC Ala	ACA Thr	GAC Asp	CTG Leu 535	GAT Asp	GCC Ala	CGC Arg	ATG Met	CAT His 540	GAT Asp	GGC Gly	ACG Thr	ACG Thr	1632
CCA Pro 545	CTG Leu	ATC Ile	CTG Leu	GCT Ala	GCC Ala 550	CGC Arg	CTG Leu	GCC Ala	GTG Val	GAG Glu 555	GGC Gly	ATG Met	CTG Leu	GAG Glu	GAC Asp 560	1680
CTC Leu	ATC Ile	AAC Asn	TCA Ser	CAC His 565	GCC Ala	GAC Asp	GTC Val	AAC Asn	GCC Ala 570	GTA Val	GAT Asp	GAC Asp	CTG Leu	GGC Gly 575	AAG Lys	1728
TCC Ser	GCC Ala	CTG Leu	CAC His 580	TGG Trp	GCC Ala	GCC Ala	GCC Ala	GTG Val 585	AAC Asn	AAT Asn	GTG Val	GAT Asp	GCC Ala 590	GCA Ala	GTT Val	1776
GTG Val	CTC Leu	CTG Leu 595	AAG Lys	AAC Asn	GGG Gly	GCT Ala	AAC Asn 600	AAA Lys	GAT Asp	ATG Met	CAG Gln	AAC Asn 605	AAC Asn	AGG Arg	GAG Glu	1824

GAG Glu	ACA Thr 610	CCC Pro	CTG Leu	TTT Phe	CTG Leu	GCC Ala 615	GCC Ala	CGG Arg	GAG Glu	GGC Gly	AGC Ser 620	TAC Tyr	GAG Glu	ACC Thr	GCC Ala	1872
AAG Lys 625	GTG Val	CTG Leu	CTG Leu	GAC Asp	CAC His 630	TTT Phe	GCC Ala	AAC Asn	CGG Arg	GAC Asp 635	ATC Ile	ACG Thr	GAT Asp	CAT His	ATG Met 640	1920
GAC Asp	CGC Arg	CTG Leu	CCG Pro	CGC Arg 645	GAC Asp	ATC Ile	GCA Ala	CAG Gln	GAG Glu 650	CGC Arg	ATG Met	CAT His	CAC His	GAC Asp 655	ATC Ile	1968
GTG Val	AGG Arg	CTG Leu	CTG Leu 660	GAC Asp	GAG Glu	TAC Tyr	AAC Asn	CTG Leu 665	GTG Val	CGC Arg	AGC Ser	CCG Pro	CAG Gln 670	CTG Leu	CAC His	2016
GGA Gly	GCC Ala	CCG Pro 675	CTG Leu	GGG Gly	GGC Gly	ACG Thr	CCC Pro 680	ACC Thr	CTG Leu	TCG Ser	CCC Pro 685	CCG Pro	CTC Leu	TGC Cys	TCG Ser	2064
CCC Pro 690	AAC Asn	GGC Gly	TAC Tyr	CTG Leu	GGC Gly	AGC Ser 695	CTC Leu	AAG Lys	CCC Pro	GGC Gly	GTG Val 700	CAG Gln	GGC Gly	AAG Lys	AAG Lys	2112
GTC Val 705	CGC Arg	AAG Lys	CCC Pro	AGC Ser	AGC Ser 710	AAA Lys	GGC Gly	CTG Leu	GCC Ala	TGT Cys 715	GGA Gly	AGC Ser	AAG Lys	GAG Glu	GCC Ala 720	2160
AAG Lys	GAC Asp	CTC Leu	AAG Lys	GCA Ala 725	CGG Arg	AGG Arg	AAG Lys	AAG Lys	TCC Ser 730	CAG Gln	GAT Asp	GGC Gly	AAG Lys	GGC Gly 735	TGC Cys	2208
CTG Leu	CTG Leu	GAC Asp	AGC Ser 740	TCC Ser	GGC Gly	ATG Met	CTC Leu	TCG Ser 745	CCC Pro	GTG Val	GAC Asp	TCC Ser	CTG Leu 750	GAG Glu	TCA Ser	2256
CCC Pro 785	CAT His	GGC Gly 755	TAC Tyr	CTG Leu	TCA Ser	GAC Asp 760	GTG Val	GCC Ala	TCG Ser	CCG Pro	CCA Pro 765	CTG Leu	CTG Leu	CCC Pro	TCC Ser	2304
CCG Pro 770	TTC Phe	CAG Gln	CAG Gln	TCT Ser	CCG Pro	TCC Ser 775	GTG Val	CCC Pro	CTC Leu	AAC Asn	CAC His 780	CTG Leu	CCT Pro	GGG Gly	ATG Met	2352
CCC Pro 785	GAC Asp	ACC Thr	CAC His	CTG Leu	GGC Gly 790	ATC Ile	GGG Gly	CAC His	CTG Leu	AAC Asn 795	GTG Val	GCG Ala	GCC Ala	AAG Lys	CCC Pro 800	2400
GAG Glu	ATG Met	GCG Ala	GCG Ala	CTG Leu 805	GGT Gly	GGG Gly	GGC Gly	GGC Gly	CGG Arg 810	CTG Leu	GCC Ala	TTT Phe	GAG Glu	ACT Thr 815	GGC Gly	2448
CCA Pro	CCT Pro	CGT Arg	CTC Leu 820	TCC Ser	CAC His	CTG Leu	CCT Pro	GTG Val 825	GCC Ala	TCT Ser	GGC Gly	ACC Thr	AGC Ser 830	ACC Thr	GTC Val	2496
CTG Leu	GGC Gly	TCC Ser 835	AGC Ser	AGC Ser	GGA Gly	GGG Gly	GCC Ala 840	CTG Leu	AAT Asn	TTC Phe	ACT Thr	GTG Val 845	GGC Gly	GGG Gly	TCC Ser	2544
ACC Thr 850	AGT Ser	TTG Leu	AAT Asn	GGT Gly	CAA Gln	TGC Cys 855	GAG Glu	TGG Trp	CTG Leu	TCC Ser	CGG Arg 860	CTG Leu	CAG Gln	AGC Ser	GGC Gly	2592
ATG Met 865	GTG Val	CCG Pro	AAC Asn	CAA Gln	TAC Tyr 870	AAC Asn	CCT Pro	CTG Leu	CGG Arg	GGG Gly 875	AGT Ser	GTG Val	GCA Ala	CCA Pro	GGC Gly 880	2640

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CCC	CTG	AGC	ACA	CAG	GCC	CCC	TCC	CTG	CAG	CAT	GGC	ATG	GTA	GGC	CCG	2688
Pro	Leu	Ser	Thr	Gln	Ala	Pro	Ser	Leu	Gln	His	Gly	Met	Val	Gly	Pro	
				885					890					895		
CTG	CAC	AGT	AGC	CTT	GCT	GCC	AGC	GCC	CTG	TCC	CAG	ATG	ATG	AGC	TAC	2736
Leu	His	Ser	Ser	Leu	Ala	Ala	Ser	Ala	Leu	Ser	Gln	Met	Met	Ser	Tyr	
			900					905					910			
CAG	GGC	CTG	CCC	AGC	ACC	CGG	CTG	GCC	ACC	CAG	CCT	CAC	CTG	GTG	CAG	2784
Gln	Gly	Leu	Pro	Ser	Thr	Arg	Leu	Ala	Thr	Gln	Pro	His	Leu	Val	Gln	
		915					920					925				
ACC	CAG	CAG	GTG	CAG	CCA	CAA	AAC	TTA	CAG	ATG	CAG	CAG	CAG	AAC	CTG	2832
Thr	Gln	Gln	Val	Gln	Pro	Gln	Asn	Leu	Gln	Met	Gln	Gln	Gln	Asn	Leu	
	930					935				940						
CAG	CCA	GCA	AAC	ATC	CAG	CAG	CAG	CAA	AGC	CTG	CAG	CCG	CCA	CCA	CCA	2880
Gln	Pro	Ala	Asn	Ile	Gln	Gln	Gln	Gln	Ser	Leu	Gln	Pro	Pro	Pro	Pro	
945					950					955					960	
CCA	CCA	CAG	CCG	CAC	CTT	GGC	GTG	AGC	TCA	GCA	GCC	AGC	GGC	CAC	CTG	2928
Pro	Pro	Gln	Pro	His	Leu	Gly	Val	Ser	Ser	Ala	Ala	Ser	Gly	His	Leu	
				965				970						975		
GGC	CGG	AGC	TTC	CTG	AGT	GGA	GAG	CCG	AGC	CAG	GCA	GAC	GTG	CAG	CCA	2976
Gly	Arg	Ser	Phe	Leu	Ser	Gly	Glu	Pro	Ser	Gln	Ala	Asp	Val	Gln	Pro	
			980					985					990			
CTG	GGC	CCC	AGC	AGC	CTG	GCG	GTG	CAC	ACT	ATT	CTG	CCC	CAG	GAG	AGC	3024
Leu	Gly	Pro	Ser	Ser	Leu	Ala	Val	His	Thr	Ile	Leu	Pro	Gln	Glu	Ser	
		995				1000						1005				
CCC	GCC	CTG	CCC	ACG	TCG	CTG	CCA	TCC	TCG	CTG	GTC	CCA	CCC	GTG	ACC	3072
Pro	Ala	Leu	Pro	Thr	Ser	Leu	Pro	Ser	Ser	Leu	Val	Pro	Pro	Val	Thr	
	1010					1015					1020					
GCA	GCC	CAG	TTC	CTG	ACG	CCC	CCC	TCG	CAG	CAC	AGC	TAC	TCC	TCG	CCT	3120
Ala	Ala	Gln	Phe	Leu	Thr	Pro	Pro	Ser	Gln	His	Ser	Tyr	Ser	Ser	Pro	
1025					1030					1035					1040	
GTG	GAC	AAC	ACC	CCC	AGC	CAC	CAG	CTA	CAG	GTG	CCT	GTT	CCT	GTA	ATG	3168
Val	Asp	Asn	Thr	Pro	Ser	His	Gln	Leu	Gln	Val	Pro	Val	Pro	Val	Met	
				1045				1050						1055		
GTA	ATG	ATC	CGA	TCT	TCG	GAT	CCT	TCT	AAA	GGC	TCA	TCA	ATT	TTG	ATC	3216
Val	Met	Ile	Arg	Ser	Ser	Asp	Pro	Ser	Lys	Gly	Ser	Ser	Ile	Leu	Ile	
			1060					1065					1070			
GAA	GCT	CCC	GAC	TCA	TGG											3234
Glu	Ala	Pro	Asp	Ser	Trp											
		1075														

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1078 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Cys	Gln	Glu	Asp	Ala	Gly	Asn	Lys	Val	Cys	Ser	Leu	Gln	Cys	Asn	Asn
1				5					10					15	

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His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp
 20 25 30
 Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser
 35 40 45
 Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp
 50 55 60
 Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp
 65 70 75 80
 Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys
 85 90 95
 Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val
 100 105 110
 Pro Glu Arg Leu Ala Ala Gly Thr Leu Val Val Val Val Leu Met Pro
 115 120 125
 Pro Glu Gln Leu Arg Asn Ser Ser Phe His Phe Leu Arg Glu Leu Ser
 130 135 140
 Arg Val Leu His Thr Asn Val Val Phe Lys Arg Asp Ala His Gly Gln
 145 150 155 160
 Gln Met Ile Phe Pro Tyr Tyr Gly Arg Glu Glu Glu Leu Arg Lys His
 165 170 175
 Pro Ile Lys Arg Ala Ala Glu Gly Trp Ala Ala Pro Asp Ala Leu Leu
 180 185 190
 Gly Gln Val Lys Ala Ser Leu Leu Pro Gly Gly Ser Glu Gly Gly Arg
 195 200 205
 Arg Arg Arg Glu Leu Asp Pro Met Asp Val Arg Gly Ser Ile Val Tyr
 210 215 220
 Leu Glu Ile Asp Asn Arg Gln Cys Val Gln Ala Ser Ser Gln Cys Phe
 225 230 235 240
 Gln Ser Ala Thr Asp Val Ala Ala Phe Leu Gly Ala Leu Ala Ser Leu
 245 250 255
 Gly Ser Leu Asn Ile Pro Tyr Lys Ile Glu Ala Val Gln Ser Glu Thr
 260 265 270
 Val Glu Pro Pro Pro Pro Ala Gln Leu His Phe Met Tyr Val Ala Ala
 275 280 285
 Ala Ala Phe Val Leu Leu Phe Phe Val Gly Cys Gly Val Leu Leu Ser
 290 295 300
 Arg Lys Arg Arg Arg Gln His Gly Gln Leu Trp Phe Pro Glu Gly Phe
 305 310 315 320
 Lys Val Ser Glu Ala Ser Lys Lys Lys Arg Arg Glu Pro Leu Gly Glu
 325 330 335
 Asp Ser Val Gly Leu Lys Pro Leu Lys Asn Ala Ser Asp Gly Ala Leu
 340 345 350
 Met Asp Asp Asn Gln Asn Glu Trp Gly Asp Glu Asp Leu Glu Thr Lys
 355 360 365
 Lys Phe Arg Phe Glu Glu Pro Val Val Leu Pro Asp Leu Asp Asp Gln

B

110

370 375 380

Thr Asp His Arg Gln Trp Thr Gln Gln His Leu Asp Ala Ala Asp Leu
385 390 395 400

Arg Met Ser Ala Met Ala Pro Thr Pro Pro Gln Gly Glu Val Asp Ala
405 410 415

Asp Cys Met Asp Val Asn Val Arg Gly Pro Asp Gly Phe Thr Pro Leu
420 425 430

Met Ile Ala Ser Cys Ser Gly Gly Gly Leu Glu Thr Gly Asn Ser Glu
435 440 445

Glu Glu Glu Asp Ala Pro Ala Val Ile Ser Asp Phe Ile Tyr Gln Gly
450 455 460

Ala Ser Leu His Asn Gln Thr Asp Arg Thr Gly Glu Thr Ala Leu His
465 470 475 480

Leu Ala Ala Arg Tyr Ser Arg Ser Asp Ala Ala Lys Arg Leu Leu Glu
485 490 495

Ala Ser Ala Asp Ala Asn Ile Gln Asp Asn Met Gly Arg Thr Pro Leu
500 505 510

His Ala Ala Val Ser Ala Asp Ala Gln Gly Val Phe Gln Ile Leu Ile
515 520 525

Arg Asn Arg Ala Thr Asp Leu Asp Ala Arg Met His Asp Gly Thr Thr
530 535 540

Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu Gly Met Leu Glu Asp
545 550 555 560

Leu Ile Asn Ser His Ala Asp Val Asn Ala Val Asp Asp Leu Gly Lys
565 570 575

Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn Val Asp Ala Ala Val
580 585 590

Val Leu Leu Lys Asn Gly Ala Asn Lys Asp Met Gln Asn Asn Arg Glu
595 600 605

Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly Ser Tyr Glu Thr Ala
610 615 620

Lys Val Leu Leu Asp His Phe Ala Asn Arg Asp Ile Thr Asp His Met
625 630 635 640

Asp Arg Leu Pro Arg Asp Ile Ala Gln Glu Arg Met His His Asp Ile
645 650 655

Val Arg Leu Leu Asp Glu Tyr Asn Leu Val Arg Ser Pro Gln Leu His
660 665 670

Gly Ala Pro Leu Gly Gly Thr Pro Thr Leu Ser Pro Pro Leu Cys Ser
675 680 685

Pro Asn Gly Tyr Leu Gly Ser Leu Lys Pro Gly Val Gln Gly Lys Lys
690 695 700

Val Arg Lys Pro Ser Ser Lys Gly Leu Ala Cys Gly Ser Lys Glu Ala
705 710 715 720

Lys Asp Leu Lys Ala Arg Arg Lys Lys Ser Gln Asp Gly Lys Gly Cys
725 730 735

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Leu Leu Asp Ser Ser Gly Met Leu Ser Pro Val Asp Ser Leu Glu Ser
 740 745 750
 Pro His Gly Tyr Leu Ser Asp Val Ala Ser Pro Pro Leu Leu Pro Ser
 755 760 765
 Pro Phe Gln Gln Ser Pro Ser Val Pro Leu Asn His Leu Pro Gly Met
 770 775 780
 Pro Asp Thr His Leu Gly Ile Gly His Leu Asn Val Ala Ala Lys Pro
 785 790 795 800
 Glu Met Ala Ala Leu Gly Gly Gly Gly Arg Leu Ala Phe Glu Thr Gly
 805 810 815
 Pro Pro Arg Leu Ser His Leu Pro Val Ala Ser Gly Thr Ser Thr Val
 820 825 830
 Leu Gly Ser Ser Ser Gly Gly Ala Leu Asn Phe Thr Val Gly Gly Ser
 835 840 845
 Thr Ser Leu Asn Gly Gln Cys Glu Trp Leu Ser Arg Leu Gln Ser Gly
 850 855 860
 Met Val Pro Asn Gln Tyr Asn Pro Leu Arg Gly Ser Val Ala Pro Gly
 865 870 875 880
 Pro Leu Ser Thr Gln Ala Pro Ser Leu Gln His Gly Met Val Gly Pro
 885 890 895
 Leu His Ser Ser Leu Ala Ala Ser Ala Leu Ser Gln Met Met Ser Tyr
 900 905 910
 Gln Gly Leu Pro Ser Thr Arg Leu Ala Thr Gln Pro His Leu Val Gln
 915 920 925
 Thr Gln Gln Val Gln Pro Gln Asn Leu Gln Met Gln Gln Gln Asn Leu
 930 935 940
 Gln Pro Ala Asn Ile Gln Gln Gln Gln Ser Leu Gln Pro Pro Pro Pro
 945 950 955 960
 Pro Pro Gln Pro His Leu Gly Val Ser Ser Ala Ala Ser Gly His Leu
 965 970 975
 Gly Arg Ser Phe Leu Ser Gly Glu Pro Ser Gln Ala Asp Val Gln Pro
 980 985 990
 Leu Gly Pro Ser Ser Leu Ala Val His Thr Ile Leu Pro Gln Glu Ser
 995 1000 1005
 Pro Ala Leu Pro Thr Ser Leu Pro Ser Ser Leu Val Pro Pro Val Thr
 1010 1015 1020
 Ala Ala Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro
 1025 1030 1035 1040
 Val Asp Asn Thr Pro Ser His Gln Leu Gln Val Pro Val Pro Val Met
 1045 1050 1055
 Val Met Ile Arg Ser Ser Asp Pro Ser Lys Gly Ser Ser Ile Leu Ile
 1060 1065 1070
 Glu Ala Pro Asp Ser Trp
 1075

(2) INFORMATION FOR SEQ ID NO:12:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4268 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..1972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

G	GAG	GTG	GAT	GTG	TTA	GAT	GTG	AAT	GTC	CGT	GGC	CCA	GAT	GGC	TGC		46
	Glu	Val	Asp	Val	Leu	Asp	Val	Asn	Val	Arg	Gly	Pro	Asp	Gly	Cys		
	1				5				10					15			
ACC	CCA	TTG	ATG	TTG	GCT	TCT	CTC	CGA	GGA	GGC	AGC	TCA	GAT	TTG	AGT		94
Thr	Pro	Leu	Met	Leu	Ala	Ser	Leu	Arg	Gly	Gly	Ser	Ser	Asp	Leu	Ser		
				20					25					30			
GAT	GAA	GAT	GAA	GAT	GCA	GAG	GAC	TCT	TCT	GCT	AAC	ATC	ATC	ACA	GAC		142
Asp	Glu	Asp	Glu	Asp	Ala	Glu	Asp	Ser	Ser	Ala	Asn	Ile	Ile	Thr	Asp		
			35					40					45				
TTG	GTC	TAC	CAG	GGT	GCC	AGC	CTC	CAG	GCC	CAG	ACA	GAC	CGG	ACT	GGT		190
Leu	Val	Tyr	Gln	Gly	Ala	Ser	Leu	Gln	Ala	Gln	Thr	Asp	Arg	Thr	Gly		
		50					55					60					
GAG	ATG	GCC	CTG	CAC	CTT	GCA	GCC	CGC	TAC	TCA	CGG	GCT	GAT	GCT	GCC		238
Glu	Met	Ala	Leu	His	Leu	Ala	Ala	Arg	Tyr	Ser	Arg	Ala	Asp	Ala	Ala		
	65					70					75						
AAG	CGT	CTC	CTG	GAT	GCA	GGT	GCA	GAT	GCC	AAT	GCC	CAG	GAC	AAC	ATG		286
Lys	Arg	Leu	Leu	Asp	Ala	Gly	Ala	Asp	Ala	Asn	Ala	Gln	Asp	Asn	Met		
	80				85				90						95		
GGC	CGC	TGT	CCA	CTC	CAT	GCT	GCA	GTG	GCA	GCT	GAT	GCC	CAA	GGT	GTC		334
Gly	Arg	Cys	Pro	Leu	His	Ala	Ala	Val	Ala	Ala	Asp	Ala	Gln	Gly	Val		
				100				105						110			
TTC	CAG	ATT	CTG	ATT	CGC	AAC	CGA	GTA	ACT	GAT	CTA	GAT	GCC	AGG	ATG		382
Phe	Gln	Ile	Leu	Ile	Arg	Asn	Arg	Val	Thr	Asp	Leu	Asp	Ala	Arg	Met		
			115					120					125				
AAT	GAT	GGT	ACT	ACA	CCC	CTG	ATC	CTG	GCT	GCC	CGC	CTG	GCT	GTG	GAG		430
Asn	Asp	Gly	Thr	Thr	Pro	Leu	Ile	Leu	Ala	Ala	Arg	Leu	Ala	Val	Glu		
		130					135					140					
GGA	ATG	GTG	GCA	GAA	CTG	ATC	AAC	TGC	CAA	GCG	GAT	GTG	AAT	GCA	GTG		478
Gly	Met	Val	Ala	Glu	Leu	Ile	Asn	Cys	Gln	Ala	Asp	Val	Asn	Ala	Val		
	145					150					155						
GAT	GAC	CAT	GGA	AAA	TCT	GCT	CTT	CAC	TGG	GCA	GCT	GCT	GTC	AAT	AAT		526
Asp	Asp	His	Gly	Lys	Ser	Ala	Leu	His	Trp	Ala	Ala	Ala	Val	Asn	Asn		
	160				165				170						175		
GTG	GAG	GCA	ACT	CTT	TTG	TTG	TTG	AAA	AAT	GGG	GCC	AAC	CGA	GAC	ATG		574
Val	Glu	Ala	Thr	Leu	Leu	Leu	Leu	Lys	Asn	Gly	Ala	Asn	Arg	Asp	Met		
				180				185						190			
CAG	GAC	AAC	AAG	GAA	GAG	ACA	CCT	CTG	TTT	CTT	GCT	GCC	CGG	GAG	GGG		622
Gln	Asp	Asn	Lys	Glu	Glu	Thr	Pro	Leu	Phe	Leu	Ala	Ala	Arg	Glu	Gly		
			195					200					205				

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AGC Ser	TAT Tyr	GAA Glu 210	GCA Ala	GCC Ala	AAG Lys	ATC Ile	CTG Leu 215	TTA Leu	GAC Asp	CAT His	TTT Phe	GCC Ala 220	AAT Asn	CGA Arg	GAC Asp	670
ATC Ile	ACA Thr 225	GAC Asp	CAT His	ATG Met	GAT Asp	CGT Arg 230	CTT Leu	CCC Pro	CGG Arg	GAT Asp	GTG Val 235	GCT Ala	CGG Arg	GAT Asp	CGC Arg	718
ATG Met 240	CAC His	CAT His	GAC Asp	ATT Ile	GTG Val 245	CGC Arg	CTT Leu	CTG Leu	GAT Asp	GAA Glu 250	TAC Tyr	AAT Asn	GTG Val	ACC Thr	CCA Pro 255	766
AGC Ser	CCT Pro	CCA Pro	GGC Gly	ACC Thr 260	GTG Val	TTG Leu	ACT Thr	TCT Ser	GCT Ala 265	CTC Leu	TCA Ser	CCT Pro	GTC Val	ATC Ile 270	TGT Cys	814
GGG Gly	CCC Pro	AAC Asn 275	AGA Arg	TCT Ser	TTC Phe	CTC Leu	AGC Ser 280	CTG Leu	AAG Lys	CAC His	ACC Thr	CCA Pro	ATG Met 285	GGC Gly	AAG Lys	862
AAG Lys	TCT Ser 290	AGA Arg	CGG Arg	CCC Pro	AGT Ser	GCC Ala	AAG Lys 295	AGT Ser	ACC Thr	ATG Met	CCT Pro	ACT Thr 300	AGC Ser	CTC Leu	CCT Pro	910
AAC Asn 305	CTT Leu	GCC Ala	AAG Lys	GAG Glu	GCA Ala	AAG Lys 310	GAT Asp	GCC Ala	AAG Lys	GGT Gly	AGT Ser 315	AGG Arg	AGG Arg	AAG Lys	AAG Lys	958
TCT Ser 320	CTG Leu	AGT Ser	GAG Glu	AAG Lys	GTC Val 325	CAA Gln	CTG Leu	TCT Ser	GAG Glu	AGT Ser 330	TCA Ser	GTA Val	ACT Thr	TTA Leu	TCC Ser 335	1006
CCT Pro	GTT Val	GAT Asp	TCC Ser 340	CTA Leu	GAA Glu	TCT Ser	CCT Pro	CAC His	ACG Thr 345	TAT Tyr	GTT Val	TCC Ser	GAC Asp	ACC Thr 350	ACA Thr	1054
TCC Ser	TCT Ser	CCA Pro	ATG Met 355	ATT Ile	ACA Thr	TCC Ser	CCT Pro	GGG Gly 360	ATC Ile	TTA Leu	CAG Gln	GCC Ala 365	TCA Ser	CCC Pro	AAC Asn	1102
CCT Pro	ATG Met 370	TTG Leu	GCC Ala	ACT Thr	GCC Ala	GCC Ala	CCT Pro 375	CCT Pro	GCC Ala	CCA Pro	GTC Val	CAT His 380	GCC Ala	CAG Gln	CAT His	1150
GCA Ala 385	CTA Leu	TCT Ser	TTT Phe	TCT Ser	AAC Asn	CTT Leu 390	CAT His	GAA Glu	ATG Met	CAG Gln	CCT Pro 395	TTG Leu	GCA Ala	CAT His	GGG Gly	1198
GCC Ala 400	AGC Ser	ACT Thr	GTG Val	CTT Leu	CCC Pro 405	TCA Ser	GTG Val	AGC Ser	CAG Gln	TTG Leu 410	CTA Leu	TCC Ser	CAC His	CAC His	CAC His 415	1246
ATT Ile	GTG Val	TCT Ser	CCA Pro	GGC Gly 420	AGT Ser	GGC Gly	AGT Ser	GCT Ala	GGA Gly 425	AGC Ser	TTG Leu	AGT Ser	AGG Arg	CTC Leu 430	CAT His	1294
CCA Pro	GTC Val	CCA Pro	GTC Val 435	CCA Pro	GCA Ala	GAT Asp	TGG Trp 440	ATG Met	AAC Asn	CGC Arg	ATG Met	GAG Glu 445	GTG Val	AAT Asn	GAG Glu	1342
ACC Thr	CAG Gln 450	TAC Tyr	AAT Asn	GAG Glu	ATG Met	TTT Phe	GGT Gly 455	ATG Met	GTC Val	CTG Leu	GCT Ala 460	CCA Pro	GCT Ala	GAG Glu	GGC Gly	1390
ACC Thr 465	CAT His	CCT Pro	GGC Gly	ATA Ile	GCT Ala	CCC Pro 470	CAG Gln	AGC Ser	AGG Arg	CCA Pro	CCT Pro 475	GAA Glu	GGG Gly	AAG Lys	CAC His	1438

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ATA	ACC	ACC	CCT	CGG	GAG	CCC	TTG	CCC	CCC	ATT	GTG	ACT	TTC	CAG	CTC	1486
Ile	Thr	Thr	Pro	Arg	Glu	Pro	Leu	Pro	Pro	Ile	Val	Thr	Phe	Gln	Leu	
480					485					490					495	
ATC	CCT	AAA	GGC	AGT	ATT	GCC	CAA	CCA	GCG	GGG	GCT	CCC	CAG	CCT	CAG	1534
Ile	Pro	Lys	Gly	Ser	Ile	Ala	Gln	Pro	Ala	Gly	Ala	Pro	Gln	Pro	Gln	
				500					505					510		
TCC	ACC	TGC	CCT	CCA	GCT	GTT	GCG	GGC	CCC	CTG	CCC	ACC	ATG	TAC	CAG	1582
Ser	Thr	Cys	Pro	Pro	Ala	Val	Ala	Gly	Pro	Leu	Pro	Thr	Met	Tyr	Gln	
			515					520					525			
ATT	CCA	GAA	ATG	GCC	CGT	TTG	CCC	AGT	GTG	GCT	TTC	CCC	ACT	GCC	ATG	1630
Ile	Pro	Glu	Met	Ala	Arg	Leu	Pro	Ser	Val	Ala	Phe	Pro	Thr	Ala	Met	
		530					535					540				
ATG	CCC	CAG	CAG	GAC	GGG	CAG	GTA	GCT	CAG	ACC	ATT	CTC	CCA	GCC	TAT	1678
Met	Pro	Gln	Gln	Asp	Gly	Gln	Val	Ala	Gln	Thr	Ile	Leu	Pro	Ala	Tyr	
	545					550					555					
CAT	CCT	TTC	CCA	GCC	TCT	GTG	GGC	AAG	TAC	CCC	ACA	CCC	CCT	TCA	CAG	1726
His	Pro	Phe	Pro	Ala	Ser	Val	Gly	Lys	Tyr	Pro	Thr	Pro	Pro	Ser	Gln	
560					565					570					575	
CAC	AGT	TAT	GCT	TCC	TCA	AAT	GCT	GCT	GAG	CGA	ACA	CCC	AGT	CAC	AGT	1774
His	Ser	Tyr	Ala	Ser	Ser	Asn	Ala	Ala	Glu	Arg	Thr	Pro	Ser	His	Ser	
				580					585					590		
GGT	CAC	CTC	CAG	GGT	GAG	CAT	CCC	TAC	CTG	ACA	CCA	TCC	CCA	GAG	TCT	1822
Gly	His	Leu	Gln	Gly	Glu	His	Pro	Tyr	Leu	Thr	Pro	Ser	Pro	Glu	Ser	
			595					600					605			
CCT	GAC	CAG	TGG	TCA	AGT	TCA	TCA	CCC	CAC	TCT	GCT	TCT	GAC	TGG	TCA	1870
Pro	Asp	Gln	Trp	Ser	Ser	Ser	Ser	Pro	His	Ser	Ala	Ser	Asp	Trp	Ser	
		610					615					620				
GAT	GTG	ACC	ACC	AGC	CCT	ACC	CCT	GGG	GGT	GCT	GGA	GGA	GGT	CAG	CGG	1918
Asp	Val	Thr	Thr	Ser	Pro	Thr	Pro	Gly	Gly	Ala	Gly	Gly	Gly	Gln	Arg	
	625					630					635					
GGA	CCT	GGG	ACA	CAC	ATG	TCT	GAG	CCA	CCA	CAC	AAC	AAC	ATG	CAG	GTT	1966
Gly	Pro	Gly	Thr	His	Met	Ser	Glu	Pro	Pro	His	Asn	Asn	Met	Gln	Val	
640					645					650					655	
TAT	GCG	TGAGAGAGTC	CACCTCCAGT	GTAGAGACAT	AACTGACTTT	TGTAAATGCT										2022
Tyr	Ala															
GCTGAGGAAC	AAATGAAGGT	CATCCGGGAG	AGAAATGAAG	AAATCTCTGG	AGCCAGCTTC											2082
TAGAGGTAGG	AAAGAGAAGA	TGTTCTTATT	CAGATAATGC	AAGAGAAGCA	ATTCGTCAGT											2142
TTCACTGGGT	ATCTGCAAGG	CTTATTGATT	ATTCTAATCT	AATAAGACAA	GTTTGTGGAA											2202
ATGCAAGATG	AATACAAGCC	TTGGGTCCAT	GTTTACTCTC	TTCTATTGCG	AGAATAAGAT											2262
GGATGCTTAT	TGAAGCCCAG	ACATTCTTGC	AGCTTGGAAT	GCATTTTAAG	CCCTGCAGGC											2322
TTCTGCCATA	TCCATGAGAA	GATTCTACAC	TAGCGTCCTG	TTGGGAATTA	TGCCCTGGAA											2382
TTCTGCCTGA	ATTGACCTAC	GCATCTCCTC	CTCCTTGGAC	ATTCTTTTGT	CTTCATTGCG											2442
TGCTTTTGGT	TTTGACCTC	TCCGTGATTG	TAGCCCTACC	AGCATGTTAT	AGGGCAAGAC											2502
CTTTGTGCTT	TTGATCATTG	TGGCCCATGA	AAGCAACTTT	GGTCTCCTTT	CCCCTCCTGT											2562
CTTCCCGGTA	TCCCTTGGAG	TCTCACAAGG	TTTACTTTGG	TATGGTTCTC	AGCACAAACC											2622

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TTTCAAGTAT GTTGTCTTCTT TGGAAAATGG ACATACTGTA TTGTGTTCTC CTGCATATAT 2682
 CATTCTGGA GAGAGAAGGG GAGAAGAATA CTTTTCTTCA ACAAATTTTG GGGGCAGGAG 2742
 ATCCCTTCAA GAGGCTGCAC CTTAATTTTT CTTGTCTGTG TGCAGGTCTT CATATAAACT 2802
 TTACCAGGAA GAAGGGTGTG AGTTTGTTGT TTTTCTGTGT ATGGGCCTGG TCAGTGTAAG 2862
 GTTTTATCCT TGATAGTCTA GTTACTATGA CCCTCCCCAC TTTTTTAAAA CCAGAAAAAG 2922
 GTTTGGAATG TTGGAATGAC CAAGAGACAA GTTAACTCGT GCAAGAGCCA GTTACCCACC 2982
 CACAGGTCCC CCTACTTCCT GCCAAGCATT CCATTGACTG CCTGTATGGA ACACATTTGT 3042
 CCCAGATCTG AGCATTCTAG GCCTGTTTCA CTCACTCACC CAGCATATGA AACTAGTCTT 3102
 AACTGTTGAG CCTTTCCTTT CATATCCACA GAAGACACTG TCTCAAATGT TGTACCCTTG 3162
 CCATTTAGGA CTGAACTTTC CTTAGCCCAA GGGACCCAGT GACAGTTGTC TTCCGTTTGT 3222
 CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT 3282
 TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 3342
 TTATATGTTT AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC 3402
 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 3462
 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522
 AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582
 TTGTTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642
 TCTTTGACTT TCTTTTAAGG GCAGAAGCAT TTTAGTTAAT TGTAGATAAA GAATAGTTTT 3702
 CTTCTCTTTC TCCTTGGGCC AGTTAATAAT TGGTCCATGG CTACACTGCA ACTTCCGTCC 3762
 AGTGCTGTGA TGCCCATGAC ACCTGCAAAA TAAGTTCTGC CTGGGCATTT TGTAGATATT 3822
 AACAGGTGAA TTCCCGACTC TTTTGGTTTG AATGACAGTT CTCATTCCTT CTATGGCTGC 3882
 AAGTATGCAT CAGTGCTTCC CACTTACCTG ATTTGTCTGT CGGTGGCCCC ATATGGAAAC 3942
 CCTGCGTGTC TGTTGGCATA ATAGTTTACA AATGGTTTTT TCAGTCCTAT CCAAATTTAT 4002
 TGAACCAACA AAAATAATTA CTTCTGCCCT GAGATAAGCA GATTAAGTTT GTTCATTCTC 4062
 TGCTTTATTC TCTCCATGTG GCAACATTCT GTCAGCCTCT TTCATAGTGT GCAAACATTT 4122
 TATCATTCTA AATGGTGACT CTCTGCCCTT GGACCCATTT ATTATTCACA GATGGGGAGA 4182
 ACCTATCTGC ATGGACCCTC ACCATCCTCT GTGCAGCACA CACAGTGCAG GGAGCCAGTG 4242
 GCGATGGCGA TGACTTTCTT CCCCTG 4268

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 657 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys Thr
 1 5 10 15
 Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser Asp
 20 25 30
 Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp Leu
 35 40 45
 Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly Glu
 50 55 60
 Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala Lys
 65 70 75 80
 Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met Gly
 85 90 95
 Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Gln Gly Val Phe
 100 105 110
 Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met Asn
 115 120 125
 Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu Gly
 130 135 140
 Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val Asp
 145 150 155 160
 Asp His Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn Val
 165 170 175
 Glu Ala Thr Leu Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met Gln
 180 185 190
 Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly Ser
 195 200 205
 Tyr Glu Ala Ala Lys Ile Leu Leu Asp His Phe Ala Asn Arg Asp Ile
 210 215 220
 Thr Asp His Met Asp Arg Leu Pro Arg Asp Val Ala Arg Asp Arg Met
 225 230 235 240
 His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn Val Thr Pro Ser
 245 250 255
 Pro Pro Gly Thr Val Leu Thr Ser Ala Leu Ser Pro Val Ile Cys Gly
 260 265 270
 Pro Asn Arg Ser Phe Leu Ser Leu Lys His Thr Pro Met Gly Lys Lys
 275 280 285
 Ser Arg Arg Pro Ser Ala Lys Ser Thr Met Pro Thr Ser Leu Pro Asn
 290 295 300
 Leu Ala Lys Glu Ala Lys Asp Ala Lys Gly Ser Arg Arg Lys Lys Ser
 305 310 315 320
 Leu Ser Glu Lys Val Gln Leu Ser Glu Ser Ser Val Thr Leu Ser Pro
 325 330 335
 Val Asp Ser Leu Glu Ser Pro His Thr Tyr Val Ser Asp Thr Thr Ser
 340 345 350
 Ser Pro Met Ile Thr Ser Pro Gly Ile Leu Gln Ala Ser Pro Asn Pro

B

117

355					360					365					
Met	Leu	Ala	Thr	Ala	Ala	Pro	Pro	Ala	Pro	Val	His	Ala	Gln	His	Ala
	370					375					380				
Leu	Ser	Phe	Ser	Asn	Leu	His	Glu	Met	Gln	Pro	Leu	Ala	His	Gly	Ala
385					390					395					400
Ser	Thr	Val	Leu	Pro	Ser	Val	Ser	Gln	Leu	Leu	Ser	His	His	His	Ile
				405					410					415	
Val	Ser	Pro	Gly	Ser	Gly	Ser	Ala	Gly	Ser	Leu	Ser	Arg	Leu	His	Pro
			420					425					430		
Val	Pro	Val	Pro	Ala	Asp	Trp	Met	Asn	Arg	Met	Glu	Val	Asn	Glu	Thr
		435					440					445			
Gln	Tyr	Asn	Glu	Met	Phe	Gly	Met	Val	Leu	Ala	Pro	Ala	Glu	Gly	Thr
	450					455					460				
His	Pro	Gly	Ile	Ala	Pro	Gln	Ser	Arg	Pro	Pro	Glu	Gly	Lys	His	Ile
465					470					475					480
Thr	Thr	Pro	Arg	Glu	Pro	Leu	Pro	Pro	Ile	Val	Thr	Phe	Gln	Leu	Ile
				485					490					495	
Pro	Lys	Gly	Ser	Ile	Ala	Gln	Pro	Ala	Gly	Ala	Pro	Gln	Pro	Gln	Ser
			500					505					510		
Thr	Cys	Pro	Pro	Ala	Val	Ala	Gly	Pro	Leu	Pro	Thr	Met	Tyr	Gln	Ile
		515					520					525			
Pro	Glu	Met	Ala	Arg	Leu	Pro	Ser	Val	Ala	Phe	Pro	Thr	Ala	Met	Met
	530					535					540				
Pro	Gln	Gln	Asp	Gly	Gln	Val	Ala	Gln	Thr	Ile	Leu	Pro	Ala	Tyr	His
545					550					555					560
Pro	Phe	Pro	Ala	Ser	Val	Gly	Lys	Tyr	Pro	Thr	Pro	Pro	Ser	Gln	His
				565					570					575	
Ser	Tyr	Ala	Ser	Ser	Asn	Ala	Ala	Glu	Arg	Thr	Pro	Ser	His	Ser	Gly
			580					585					590		
His	Leu	Gln	Gly	Glu	His	Pro	Tyr	Leu	Thr	Pro	Ser	Pro	Glu	Ser	Pro
		595					600					605			
Asp	Gln	Trp	Ser	Ser	Ser	Ser	Pro	His	Ser	Ala	Ser	Asp	Trp	Ser	Asp
	610					615					620				
Val	Thr	Thr	Ser	Pro	Thr	Pro	Gly	Gly	Ala	Gly	Gly	Gly	Gln	Arg	Gly
625					630					635					640
Pro	Gly	Thr	His	Met	Ser	Glu	Pro	Pro	His	Asn	Asn	Met	Gln	Val	Tyr
				645					650					655	

Ala

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Asp Ile Asp Glu Cys Asp Gln Gly Ser Pro Cys Glu His Asn Gly
1 5 10 15
Ile Cys Val Asn Thr Pro Gly Ser Tyr Arg Cys Asn Cys Ser Gln Gly
20 25 30
Phe Thr Gly Pro Arg Cys Glu Thr Asn Ile Asn Glu Cys Glu Ser His
35 40 45
Pro Cys Gln Asn Glu Gly Ser Cys Leu Asp Asp Pro Gly Thr Phe Arg
50 55 60
Cys Val Cys Met Pro Gly Phe Thr Gly Thr Gln Cys Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn Asp Val Asp Glu Cys Ser Leu Gly Ala Asn Pro Cys Glu His Gly
1 5 10 15
Gly Arg Cys Thr Asn Thr Leu Gly Ser Phe Gln Cys Asn Cys Pro Gln
20 25 30
Gly Tyr Ala Gly Pro Arg Cys Glu Ile Asp Val Asn Glu Cys Leu Ser
35 40 45
Asn Pro Cys Gln Asn Asp Ser Thr Cys Leu Asp Gln Ile Gly Glu Phe
50 55 60
Gln Cys Ile Cys Met Pro Gly Tyr Glu Gly Leu Tyr Cys Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 654 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Pro Pro Gln Gly Glu Ile Glu Ala Asp Cys Met Asp Val Asn Val

119

1				5						10					15
Arg	Gly	Pro	Asp	Gly	Phe	Thr	Pro	Leu	Met	Ile	Ala	Ser	Cys	Ser	Gly
			20					25					30		
Gly	Gly	Leu	Glu	Thr	Gly	Asn	Ser	Glu	Glu	Glu	Glu	Asp	Ala	Ser	Ala
		35					40					45			
Asn	Met	Ile	Ser	Asp	Phe	Ile	Gly	Gln	Gly	Ala	Gln	Leu	His	Asn	Gln
	50					55					60				
Thr	Asp	Arg	Thr	Gly	Glu	Thr	Ala	Leu	His	Leu	Ala	Ala	Arg	Tyr	Ala
65					70					75					80
Arg	Ala	Asp	Ala	Ala	Lys	Arg	Leu	Leu	Glu	Ser	Ser	Ala	Asp	Ala	Asn
				85					90					95	
Val	Gln	Asp	Asn	Met	Gly	Arg	Thr	Pro	Leu	His	Ala	Ala	Val	Ala	Ala
			100					105					110		
Asp	Ala	Gln	Gly	Val	Phe	Gln	Ile	Leu	Ile	Arg	Asn	Arg	Ala	Thr	Asp
		115					120					125			
Leu	Asp	Ala	Arg	Met	Phe	Asp	Gly	Thr	Thr	Pro	Leu	Ile	Leu	Ala	Ala
	130					135					140				
Arg	Leu	Ala	Val	Glu	Gly	Met	Val	Glu	Glu	Leu	Ile	Asn	Ala	His	Ala
145					150					155					160
Asp	Val	Asn	Ala	Val	Asp	Glu	Phe	Gly	Lys	Ser	Ala	Leu	His	Trp	Ala
				165					170					175	
Ala	Ala	Val	Asn	Asn	Val	Asp	Ala	Ala	Ala	Val	Leu	Leu	Lys	Asn	Ser
			180					185					190		
Ala	Asn	Lys	Asp	Met	Gln	Asn	Asn	Lys	Glu	Glu	Thr	Ser	Leu	Phe	Leu
		195					200					205			
Ala	Ala	Arg	Glu	Gly	Ser	Tyr	Glu	Thr	Ala	Lys	Val	Leu	Leu	Asp	His
						215					220				
Tyr	Ala	Asn	Arg	Asp	Ile	Thr	Asp	His	Met	Asp	Arg	Leu	Pro	Arg	Asp
225					230					235					240
Ile	Ala	Gln	Glu	Arg	Met	His	His	Asp	Ile	Val	His	Leu	Leu	Asp	Glu
				245					250					255	
Tyr	Asn	Leu	Val	Lys	Ser	Pro	Thr	Leu	His	Asn	Gly	Pro	Leu	Gly	Ala
			260					265					270		
Thr	Thr	Leu	Ser	Pro	Pro	Ile	Cys	Ser	Pro	Asn	Gly	Tyr	Met	Gly	Asn
		275					280					285			
Met	Lys	Pro	Ser	Val	Gln	Ser	Lys	Lys	Ala	Arg	Lys	Pro	Ser	Ile	Lys
	290					295					300				
Gly	Asn	Gly	Cys	Lys	Glu	Ala	Lys	Glu	Leu	Lys	Ala	Arg	Arg	Lys	Lys
305					310					315					320
Ser	Gln	Asp	Gly	Lys	Thr	Thr	Leu	Leu	Asp	Ser	Gly	Ser	Ser	Gly	Val
				325					330					335	
Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Thr	His	Gly	Tyr	Leu	Ser	Asp
			340					345					350		
Val	Ser	Ser	Pro	Pro	Leu	Met	Thr	Ser	Pro	Phe	Gln	Gln	Ser	Pro	Ser
		355					360					365			

B

120

Met Pro Leu Asn His Leu Thr Ser Met Pro Glu Ser Gln Leu Gly Met
370 375 380

Asn His Ile Asn Met Ala Thr Lys Gln Glu Met Ala Ala Gly Ser Asn
385 390 395 400

Arg Met Ala Phe Asp Ala Met Val Pro Arg Leu Thr His Leu Asn Ala
405 410 415

Ser Ser Pro Asn Thr Ile Met Ser Asn Gly Ser Met His Phe Thr Val
420 425 430

Gly Gly Ala Pro Thr Met Asn Ser Gln Cys Asp Trp Leu Ala Arg Leu
435 440 445

Gln Asn Gly Met Val Gln Asn Gln Tyr Asp Pro Ile Arg Asn Gly Ile
450 455 460

Gln Gln Gly Asn Ala Gln Gln Ala Gln Ala Leu Gln His Gly Leu Met
465 470 475 480

Thr Ser Leu His Asn Gly Leu Pro Ala Thr Thr Leu Ser Gln Met Met
485 490 495

Thr Tyr Gln Ala Met Pro Asn Thr Arg Leu Ala Asn Gln Pro His Leu
500 505 510

Met Gln Ala Gln Gln Met Gln Gln Gln Gln Asn Leu Gln Leu His Gln
515 520 525

Ser Met Gln Gln Gln His His Asn Ser Ser Thr Thr Ser Thr His Ile
530 535 540

Asn Ser Pro Phe Cys Ser Ser Asp Ile Ser Gln Thr Asp Leu Gln Gln
545 550 555 560

Met Ser Ser Asn Asn Ile His Ser Val Met Pro Gln Asp Thr Gln Ile
565 570 575

Phe Ala Ala Ser Leu Pro Ser Asn Leu Thr Gln Ser Met Thr Thr Ala
580 585 590

Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro Met Asp
595 600 605

Asn Thr Pro Ser His Gln Leu Gln Val Pro Asp His Pro Phe Leu Thr
610 615 620

Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser
625 630 635 640

Asn Met Ser Asp Trp Ser Glu Gly Ile Ser Ser Pro Pro Thr
645 650

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

121

Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val
 1 5 10 15
 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly
 20 25 30
 Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu Glu Asp Ala Pro Ala
 35 40 45
 Val Ile Ser Asp Phe Ile Tyr Gln Gly Ala Ser Leu His Asn Gln Thr
 50 55 60
 Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala Ala Arg Tyr Ser Arg
 65 70 75 80
 Ser Asp Ala Ala Lys Arg Leu Leu Glu Ala Ser Ala Asp Ala Asn Ile
 85 90 95
 Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala Ala Val Ser Ala Asp
 100 105 110
 Ala Gln Gly Val Phe Gln Ile Leu Leu Arg Asn Arg Ala Thr Asp Leu
 115 120 125
 Asp Ala Arg Met His Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg
 130 135 140
 Leu Ala Val Glu Gly Met Leu Glu Asp Leu Ile Asn Ser His Ala Asp
 145 150 155 160
 Val Asn Ala Val Asp Asp Leu Gly Lys Ser Ala Leu His Trp Ala Ala
 165 170 175
 Ala Val Asn Asn Val Asp Ala Ala Val Val Leu Leu Lys Asn Gly Ala
 180 185 190
 Asn Lys Asp Met Gln Asn Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala
 195 200 205
 Ala Arg Glu Gly Ser Tyr Glu Thr Ala Lys Val Leu Leu Asp His Phe
 210 215 220
 Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Ile
 225 230 235 240
 Ala Gln Glu Arg Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr
 245 250 255
 Asn Leu Val Arg Ser Pro Gln Leu His Gly Thr Ala Leu Gly Gly Thr
 260 265 270
 Pro Thr Leu Ser Pro Thr Leu Cys Ser Pro Asn Gly Tyr Leu Gly Asn
 275 280 285
 Leu Lys Ser Ala Thr Gln Gly Lys Lys Ala Arg Lys Pro Ser Thr Lys
 290 295 300
 Gly Leu Ala Cys Ser Ser Lys Glu Ala Lys Asp Leu Lys Ala Arg Arg
 305 310 315 320
 Lys Lys Ser Gln Asp Gly Lys Gly Cys Leu Leu Asp Ser Ser Ser Met
 325 330 335
 Leu Ser Pro Val Asp Ser Leu Glu Ser Pro His Gly Tyr Leu Ser Asp
 340 345 350
 Val Ala Ser Pro Pro Leu Pro Ser Pro Phe Gln Gln Ser Pro Ser Met

B

122

355					360					365					
Pro	Leu	Ser	His	Leu	Pro	Gly	Met	Pro	Asp	Thr	His	Leu	Gly	Ile	Ser
	370					375					380				
His	Leu	Asn	Val	Ala	Ala	Lys	Pro	Glu	Met	Ala	Ala	Leu	Ala	Gly	Gly
	385					390					395				400
Ser	Arg	Leu	Ala	Phe	Glu	Pro	Pro	Pro	Pro	Arg	Leu	Ser	His	Leu	Pro
				405					410					415	
Val	Ala	Ser	Ser	Ala	Ser	Thr	Val	Leu	Ser	Thr	Asn	Gly	Thr	Gly	Ala
				420				425					430		
Met	Asn	Phe	Thr	Val	Gly	Ala	Pro	Ala	Ser	Leu	Asn	Gly	Gln	Cys	Glu
		435					440					445			
Trp	Leu	Pro	Arg	Leu	Gln	Asn	Gly	Met	Val	Pro	Ser	Gln	Tyr	Asn	Pro
	450					455					460				
Leu	Arg	Pro	Gly	Val	Thr	Pro	Gly	Thr	Leu	Ser	Thr	Gln	Ala	Ala	Gly
	465					470					475				480
Leu	Gln	His	Gly	Met	Met	Ser	Pro	Ile	His	Ser	Ser	Leu	Ser	Thr	Asn
				485					490					495	
Thr	Leu	Ser	Pro	Ile	Ile	Tyr	Gln	Gly	Leu	Pro	Asn	Thr	Arg	Leu	Ala
			500					505					510		
Thr	Gln	Pro	His	Leu	Val	Gln	Thr	Gln	Gln	Val	Gln	Pro	Gln	Asn	Leu
		515					520					525			
Gln	Ile	Gln	Pro	Gln	Asn	Leu	Gln	Pro	Pro	Ser	Gln	Pro	His	Leu	Ser
	530					535					540				
Val	Ser	Ser	Ala	Ala	Asn	Gly	His	Leu	Gly	Arg	Ser	Phe	Leu	Ser	Gly
	545					550					555				560
Glu	Pro	Ser	Gln	Ala	Asp	Val	Gln	Pro	Leu	Gly	Pro	Ser	Ser	Leu	Pro
				565					570					575	
Val	His	Thr	Ile	Leu	Pro	Gln	Glu	Ser	Gln	Ala	Leu	Pro	Thr	Ser	Leu
			580					585					590		
Pro	Ser	Ser	Met	Val	Pro	Pro	Met	Thr	Thr	Thr	Gln	Phe	Leu	Thr	Pro
		595					600					605			
Pro	Ser	Gln	His	Ser	Tyr	Ser	Ser	Ser	Pro	Val	Asp	Asn	Thr	Pro	Ser
	610					615					620				
His	Gln	Leu	Gln	Val	Pro	Glu	His	Pro	Phe	Leu	Thr	Pro	Ser	Pro	Glu
	625					630					635				640
Ser	Pro	Asp	Gln	Trp	Ser	Ser	Ser	Ser	Arg	His	Ser	Asn	Ile	Ser	Asp
				645					650					655	
Trp	Ser	Glu	Gly	Ile	Ser	Ser	Pro	Pro	Thr						
			660					665							

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 681 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

123

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val
1 5 10 15
Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly
20 25 30
Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu Glu Asp Ala Pro Ala
35 40 45
Val Ile Ser Asp Phe Ile Tyr Gln Gly Ala Ser Leu His Asn Gln Thr
50 55 60
Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala Ala Arg Tyr Ser Arg
65 70 75 80
Ser Asp Ala Ala Lys Arg Leu Leu Glu Ala Ser Ala Asp Ala Asn Ile
85 90 95
Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala Ala Val Ser Ala Asp
100 105 110
Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg Ala Thr Asp Leu
115 120 125
Asp Ala Arg Met His Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg
130 135 140
Leu Ala Val Glu Gly Met Leu Glu Asp Leu Ile Asn Ser His Ala Asp
145 150 155 160
Val Asn Ala Val Asp Asp Leu Gly Lys Ser Ala Leu His Trp Ala Ala
165 170 175
Ala Val Asn Asn Val Asp Ala Ala Val Val Leu Leu Lys Asn Gly Ala
180 185 190
Asn Lys Asp Met Gln Asn Asn Arg Glu Glu Thr Pro Leu Phe Leu Ala
195 200 205
Ala Arg Glu Gly Ser Tyr Glu Thr Ala Lys Val Leu Leu Asp His Phe
210 215 220
Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Ile
225 230 235 240
Ala Gln Glu Arg Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr
245 250 255
Asn Leu Val Arg Ser Pro Gln Leu His Gly Ala Pro Leu Gly Gly Thr
260 265 270
Pro Thr Leu Ser Pro Pro Leu Cys Ser Pro Asn Gly Tyr Leu Gly Ser
275 280 285
Leu Lys Pro Gly Val Gln Gly Lys Lys Val Arg Lys Pro Ser Ser Lys
290 295 300
Gly Leu Ala Cys Gly Ser Lys Glu Ala Lys Asp Leu Lys Ala Arg Arg
305 310 315 320
Lys Lys Ser Gln Asp Gly Lys Gly Cys Leu Leu Asp Ser Ser Gly Met

B

124

325								330					335				
Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	Gly	Tyr	Leu	Ser	Asp		
			340					345					350				
Val	Ala	Ser	Pro	Pro	Leu	Leu	Pro	Ser	Pro	Phe	Gln	Gln	Ser	Pro	Ser		
		355					360					365					
Val	Pro	Leu	Asn	His	Leu	Pro	Gly	Met	Pro	Asp	Thr	His	Leu	Gly	Ile		
	370					375					380						
Gly	His	Leu	Asn	Val	Ala	Ala	Lys	Pro	Glu	Met	Ala	Ala	Leu	Gly	Gly		
385					390					395					400		
Gly	Gly	Arg	Leu	Ala	Phe	Glu	Thr	Gly	Pro	Pro	Arg	Leu	Ser	His	Leu		
				405					410					415			
Pro	Val	Ala	Ser	Gly	Thr	Ser	Thr	Val	Leu	Gly	Ser	Ser	Ser	Gly	Gly		
			420					425					430				
Ala	Leu	Asn	Phe	Thr	Val	Gly	Gly	Ser	Thr	Ser	Leu	Asn	Gly	Gln	Cys		
		435					440					445					
Glu	Trp	Leu	Ser	Arg	Leu	Gln	Ser	Gly	Met	Val	Pro	Asn	Gln	Tyr	Asn		
	450					455					460						
Pro	Leu	Arg	Gly	Ser	Val	Ala	Pro	Gly	Pro	Leu	Ser	Thr	Gln	Ala	Pro		
465					470					475					480		
Ser	Leu	Gln	His	Gly	Met	Val	Gly	Pro	Leu	His	Ser	Ser	Leu	Ala	Ala		
				485					490					495			
Ser	Ala	Leu	Ser	Gln	Met	Met	Ser	Tyr	Gln	Gly	Leu	Pro	Ser	Thr	Arg		
			500					505					510				
Leu	Ala	Thr	Gln	Pro	His	Leu	Val	Gln	Thr	Gln	Gln	Val	Gln	Pro	Gln		
		515					520					525					
Asn	Leu	Gln	Met	Gln	Gln	Gln	Asn	Leu	Gln	Pro	Ala	Asn	Ile	Gln	Gln		
	530					535					540						
Gln	Gln	Ser	Leu	Gln	Pro	Pro	Pro	Pro	Pro	Pro	Gln	Pro	His	Leu	Gly		
545					550					555					560		
Val	Ser	Ser	Ala	Ala	Ser	Gly	His	Leu	Gly	Arg	Ser	Phe	Leu	Ser	Gly		
				565					570					575			
Glu	Pro	Ser	Gln	Ala	Asp	Val	Gln	Pro	Leu	Gly	Pro	Ser	Ser	Leu	Ala		
			580					585					590				
Val	His	Thr	Ile	Leu	Pro	Gln	Glu	Ser	Pro	Ala	Leu	Pro	Thr	Ser	Leu		
		595					600					605					
Pro	Ser	Ser	Leu	Val	Pro	Pro	Val	Thr	Ala	Ala	Gln	Phe	Leu	Thr	Pro		
	610					615					620						
Pro	Ser	Gln	His	Ser	Tyr	Ser	Ser	Pro	Val	Glu	Asn	Thr	Pro	Ser	His		
625					630					635					640		
Gln	Leu	Gln	Val	Pro	Glu	His	Pro	Phe	Leu	Thr	Pro	Ser	Pro	Glu	Ser		
				645					650					655			
Pro	Asp	Gln	Trp	Ser	Ser	Ser	Ser	Pro	His	Ser	Asn	Val	Ser	Asp	Trp		
			660					665					670				
Ser	Glu	Gly	Val	Ser	Ser	Pro	Pro	Thr									
		675					680										

B

125

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Pro Ala Leu Arg Pro Ala Leu Leu Trp Ala Leu Leu Ala Leu Trp
1 5 10 15

Leu Cys Cys Ala Ala Pro Ala His Ala Leu Gln Cys Arg Asp Gly Tyr
20 25 30

Glu Pro Cys Val Asn Glu Gly Met Cys Val Thr Tyr His Asn Gly Thr
35 40 45

Gly Tyr Cys Lys Cys Pro Glu Gly Phe Leu Gly Glu Tyr Cys Gln His
50 55 60

Arg Asp Pro Cys Glu Lys Asn Arg Cys Gln Asn Gly Gly Thr Cys Val
65 70 75 80

Ala Gln Ala Met Leu Gly Lys Ala Thr Cys Arg Cys Ala Ser Gly Phe
85 90 95

Thr Gly Glu Asp Cys Gln Tyr Ser Thr Ser His Pro Cys Phe Val Ser
100 105 110

Arg Pro Cys Leu Asn Gly Gly Thr Cys His Met Leu Ser Arg Asp Thr
115 120 125

Tyr Glu Cys Thr Cys Gln Val Gly Phe Thr Gly Lys Glu Cys Gln Trp
130 135 140

Thr Asp Ala Cys Leu Ser His Pro Cys Ala Asn Gly Ser Thr Cys Thr
145 150 155 160

Thr Val Ala Asn Gln Phe Ser Cys Lys Cys Leu Thr Gly Phe Thr Gly
165 170 175

Gln Lys Cys Glu Thr Asp Val Asn Glu Cys Asp Ile Pro Gly His Cys
180 185 190

Gln His Gly Gly Thr Cys Leu Asn Leu Pro Gly Ser Tyr Gln Cys Gln
195 200 205

Cys Pro Gln Gly Phe Thr Gly Gln Tyr Cys Asp Ser Leu Tyr Val Pro
210 215 220

Cys Ala Pro Ser Pro Cys Val Asn Gly Gly Thr Cys Arg Gln Thr Gly
225 230 235 240

Asp Phe Thr Phe Glu Cys Asn Cys Leu Pro Gly Phe Glu Gly Ser Thr
245 250 255

Cys Glu Arg Asn Ile Asp Asp Cys Pro Asn His Arg Cys Gln Asn Gly
260 265 270

Gly Val Cys Val Asp Gly Val Asn Thr Tyr Asn Cys Arg Cys Pro Pro
275 280 285

B

126

Gln Trp Thr Gly Gln Phe Cys Thr Glu Asp Val Asp Glu Cys Leu Leu
290 295 300

Gln Pro Asn Ala Cys Gln Asn Gly Gly Thr Cys Ala Asn Arg Asn Gly
305 310 315 320

Gly Tyr Gly Cys Val Cys Val Asn Gly Trp Ser Gly Asp Asp Cys Ser
325 330 335

Glu Asn Ile Asp Asp Cys Ala Phe Ala Ser Cys Thr Pro Gly Ser Thr
340 345 350

Cys Ile Asp Arg Val Ala Ser Phe Ser Cys Met Cys Pro Glu Gly Lys
355 360 365

Ala Gly Leu Leu Cys His Leu Asp Asp Ala Cys Ile Ser Asn Pro Cys
370 375 380

His Lys Gly Ala Leu Cys Asp Thr Asn Pro Leu Asn Gly Gln Tyr Ile
385 390 395 400

Cys Thr Cys Pro Gln Gly Tyr Lys Gly Ala Asp Cys Thr Glu Asp Val
405 410 415

Asp Glu Cys Ala Met Ala Asn Ser Asn Pro Cys Glu His Ala Gly Lys
420 425 430

Cys Val Asn Thr Asp Gly Ala Phe His Cys Glu Cys Leu Lys Gly Tyr
435 440 445

Ala Gly Pro Arg Cys Glu Met Asp Ile Asn Glu Cys His Ser Asp Pro
450 455 460

Cys Gln Asn Asp Ala Thr Cys Leu Asp Lys Ile Gly Gly Phe Thr Cys
465 470 475 480

Leu Cys Met Pro Gly Phe Lys Gly Val His Cys Glu Leu Glu Ile Asn
485 490 495

Glu Cys Gln Ser Asn Pro Cys Val Asn Asn Gly Gln Cys Val Asp Lys
500 505 510

Val Asn Arg Phe Gln Cys Leu Cys Pro Pro Gly Phe Thr Gly Pro Val
515 520 525

Cys Gln Ile Asp Ile Asp Asp Cys Ser Ser Thr Pro Cys Leu Asn Gly
530 535 540

Ala Lys Cys Ile Asp His Pro Asn Gly Tyr Glu Cys Gln Cys Ala Thr
545 550 555 560

Gly Phe Thr Gly Val Leu Cys Glu Glu Asn Ile Asp Asn Cys Asp Pro
565 570 575

Asp Pro Cys His His Gly Gln Cys Gln Asp Gly Ile Asp Ser Tyr Thr
580 585 590

Cys Ile Cys Asn Pro Gly Tyr Met Gly Ala Ile Cys Ser Asp Gln Ile
595 600 605

Asp Glu Cys Tyr Ser Ser Pro Cys Leu Asn Asp Gly Arg Cys Ile Asp
610 615 620

Leu Val Asn Gly Tyr Gln Cys Asn Cys Gln Pro Gly Thr Ser Gly Val
625 630 635 640

Asn Cys Glu Ile Asn Phe Asp Asp Cys Ala Ser Asn Pro Cys Ile His

645										650					655				
Gly	Ile	Cys	Met	Asp	Gly	Ile	Asn	Arg	Tyr	Ser	Cys	Val	Cys	Ser	Pro				
			660					665					670						
Gly	Phe	Thr	Gly	Gln	Arg	Cys	Asn	Ile	Asp	Ile	Asp	Glu	Cys	Ala	Ser				
		675					680					685							
Asn	Pro	Cys	Arg	Lys	Gly	Ala	Thr	Cys	Ile	Asn	Gly	Val	Asn	Gly	Phe				
	690					695					700								
Arg	Cys	Ile	Cys	Pro	Glu	Gly	Pro	His	His	Pro	Ser	Cys	Tyr	Ser	Gln				
705					710					715					720				
Val	Asn	Glu	Cys	Leu	Ser	Asn	Pro	Cys	Ile	His	Gly	Asn	Cys	Thr	Gly				
				725					730					735					
Gly	Leu	Ser	Gly	Tyr	Lys	Cys	Leu	Cys	Asp	Ala	Gly	Trp	Val	Gly	Ile				
			740					745					750						
Asn	Cys	Glu	Val	Asp	Lys	Asn	Glu	Cys	Leu	Ser	Asn	Pro	Cys	Gln	Asn				
		755					760					765							
Gly	Gly	Thr	Cys	Asp	Asn	Leu	Val	Asn	Gly	Tyr	Arg	Cys	Thr	Cys	Lys				
	770					775					780								
Lys	Gly	Phe	Lys	Gly	Tyr	Asn	Cys	Gln	Val	Asn	Ile	Asp	Glu	Cys	Ala				
785					790					795					800				
Ser	Asn	Pro	Cys	Leu	Asn	Gln	Gly	Thr	Cys	Phe	Asp	Asp	Ile	Ser	Gly				
				805				810					815						
Tyr	Thr	Cys	His	Cys	Val	Leu	Pro	Tyr	Thr	Gly	Lys	Asn	Cys	Gln	Thr				
			820					825					830						
Val	Leu	Ala	Pro	Cys	Ser	Pro	Asn	Pro	Cys	Glu	Asn	Ala	Ala	Val	Cys				
		835					840					845							
Lys	Glu	Ser	Pro	Asn	Phe	Glu	Ser	Tyr	Thr	Cys	Leu	Cys	Ala	Pro	Gly				
	850					855					860								
Trp	Gln	Gly	Gln	Arg	Cys	Thr	Ile	Asp	Ile	Asp	Glu	Cys	Ile	Ser	Lys				
865					870					875					880				
Pro	Cys	Met	Asn	His	Gly	Leu	Cys	His	Asn	Thr	Gln	Gly	Ser	Tyr	Met				
				885					890					895					
Cys	Glu	Cys	Pro	Pro	Gly	Phe	Ser	Gly	Met	Asp	Cys	Glu	Glu	Asp	Ile				
			900					905					910						
Asp	Asp	Cys	Leu	Ala	Asn	Pro	Cys	Gln	Asn	Gly	Gly	Ser	Cys	Met	Asp				
		915					920					925							
Gly	Val	Asn	Thr	Phe	Ser	Cys	Leu	Cys	Leu	Pro	Gly	Phe	Thr	Gly	Asp				
	930					935					940								
Lys	Cys	Gln	Thr	Asp	Met	Asn	Glu	Cys	Leu	Ser	Glu	Pro	Cys	Lys	Asn				
945					950					955					960				
Gly	Gly	Thr	Cys	Ser	Asp	Tyr	Val	Asn	Ser	Tyr	Thr	Cys	Lys	Cys	Gln				
				965					970					975					
Ala	Gly	Phe	Asp	Gly	Val	His	Cys	Glu	Asn	Asn	Ile	Asn	Glu	Cys	Thr				
			980					985					990						
Glu	Ser	Ser	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Val	Asp	Gly	Ile	Asn	Ser				
		995					1000					1005							

Phe Ser Cys Leu Cys Pro Val Gly Phe Thr Gly Ser Phe Cys Leu His
 1010 1015 1020
 Glu Ile Asn Glu Cys Ser Ser His Pro Cys Leu Asn Glu Gly Thr Cys
 1025 1030 1035 1040
 Val Asp Gly Leu Gly Thr Tyr Arg Cys Ser Cys Pro Leu Gly Tyr Thr
 1045 1050 1055
 Gly Lys Asn Cys Gln Thr Leu Val Asn Leu Cys Ser Arg Ser Pro Cys
 1060 1065 1070
 Lys Asn Lys Gly Thr Cys Val Gln Lys Lys Ala Glu Ser Gln Cys Leu
 1075 1080 1085
 Cys Pro Ser Gly Trp Ala Gly Ala Tyr Cys Asp Val Pro Asn Val Ser
 1090 1095 1100
 Cys Asp Ile Ala Ala Ser Arg Arg Gly Val Leu Val Glu His Leu Cys
 1105 1110 1115 1120
 Gln His Ser Gly Val Cys Ile Asn Ala Gly Asn Thr His Tyr Cys Gln
 1125 1130 1135
 Cys Pro Leu Gly Tyr Thr Gly Ser Tyr Cys Glu Glu Gln Leu Asp Glu
 1140 1145 1150
 Cys Ala Ser Asn Pro Cys Gln His Gly Ala Thr Cys Ser Asp Phe Ile
 1155 1160 1165
 Gly Gly Tyr Arg Cys Glu Cys Val Pro Gly Tyr Gln Gly Val Asn Cys
 1170 1175 1180
 Glu Tyr Glu Val Asp Glu Cys Gln Asn Gln Pro Cys Gln Asn Gly Gly
 1185 1190 1195 1200
 Thr Cys Ile Asp Leu Val Asn His Phe Lys Cys Ser Cys Pro Pro Gly
 1205 1210 1215
 Thr Arg Gly Leu Leu Cys Glu Glu Asn Ile Asp Asp Cys Ala Arg Gly
 1220 1225 1230
 Pro His Cys Leu Asn Gly Gly Gln Cys Met Asp Arg Ile Gly Gly Tyr
 1235 1240 1245
 Ser Cys Arg Cys Leu Pro Gly Phe Ala Gly Glu Arg Cys Glu Gly Asp
 1250 1255 1260
 Ile Asn Glu Cys Leu Ser Asn Pro Cys Ser Ser Glu Gly Ser Leu Asp
 1265 1270 1275 1280
 Cys Ile Gln Leu Thr Asn Asp Tyr Leu Cys Val Cys Arg Ser Ala Phe
 1285 1290 1295
 Thr Gly Arg His Cys Glu Thr Phe Val Asp Val Cys Pro Gln Met Pro
 1300 1305 1310
 Cys Leu Asn Gly Gly Thr Cys Ala Val Ala Ser Asn Met Pro Asp Gly
 1315 1320 1325
 Phe Ile Cys Arg Cys Pro Pro Gly Phe Ser Gly Ala Arg Cys Gln Ser
 1330 1335 1340
 Ser Cys Gly Gln Val Lys Cys Arg Lys Gly Glu Gln Cys Val His Thr
 1345 1350 1355 1360
 Ala Ser Gly Pro Arg Cys Phe Cys Pro Ser Pro Arg Asp Cys Glu Ser

1365										1370					1375				
Gly	Cys	Ala	Ser	Ser	Pro	Cys	Gln	His	Gly	Gly	Ser	Cys	His	Pro	Gln				
			1380					1385					1390						
Arg	Gln	Pro	Pro	Tyr	Tyr	Ser	Cys	Gln	Cys	Ala	Pro	Pro	Phe	Ser	Gly				
		1395					1400					1405							
Ser	Arg	Cys	Glu	Leu	Tyr	Thr	Ala	Pro	Pro	Ser	Thr	Pro	Pro	Ala	Thr				
	1410					1415					1420								
Cys	Leu	Ser	Gln	Tyr	Cys	Ala	Asp	Lys	Ala	Arg	Asp	Gly	Val	Cys	Asp				
1425					1430					1435					1440				
Glu	Ala	Cys	Asn	Ser	His	Ala	Cys	Gln	Trp	Asp	Gly	Gly	Asp	Cys	Ser				
				1445					1450					1455					
Leu	Thr	Met	Glu	Asn	Pro	Trp	Ala	Asn	Cys	Ser	Ser	Pro	Leu	Pro	Cys				
			1460					1465					1470						
Trp	Asp	Tyr	Ile	Asn	Asn	Gln	Cys	Asp	Glu	Leu	Cys	Asn	Thr	Val	Glu				
		1475					1480					1485							
Cys	Leu	Phe	Asp	Asn	Phe	Glu	Cys	Gln	Gly	Asn	Ser	Lys	Thr	Cys	Lys				
	1490					1495					1500								
Tyr	Asp	Lys	Tyr	Cys	Ala	Asp	His	Phe	Lys	Asp	Asn	His	Cys	Asn	Gln				
1505					1510					1515					1520				
Gly	Cys	Asn	Ser	Glu	Glu	Cys	Gly	Trp	Asp	Gly	Leu	Asp	Cys	Ala	Ala				
				1525					1530					1535					
Asp	Gln	Pro	Glu	Asn	Leu	Ala	Glu	Gly	Thr	Leu	Val	Ile	Val	Val	Leu				
			1540					1545											
Met	Pro	Pro	Glu	Gln	Leu	Leu	Gln	Asp	Ala	Arg	Ser	Phe	Leu	Arg	Ala				
		1555					1560					1565							
Leu	Gly	Thr	Leu	Leu	His	Thr	Asn	Leu	Arg	Ile	Lys	Arg	Asp	Ser	Gln				
	1570					1575					1580								
Gly	Glu	Leu	Met	Val	Tyr	Pro	Tyr	Tyr	Gly	Glu	Lys	Ser	Ala	Ala	Met				
1585					1590					1595					1600				
Lys	Lys	Gln	Arg	Met	Thr	Arg	Arg	Ser	Leu	Pro	Gly	Glu	Gln	Glu	Gln				
				1605					1610					1615					
Glu	Val	Ala	Gly	Ser	Lys	Val	Phe	Leu	Glu	Ile	Asp	Asn	Arg	Gln	Cys				
			1620					1625					1630						
Val	Gln	Asp	Ser	Asp	His	Cys	Phe	Lys	Asn	Thr	Asp	Ala	Ala	Ala	Ala				
		1635					1640					1645							
Leu	Leu	Ala	Ser	His	Ala	Ile	Gln	Gly	Thr	Leu	Ser	Tyr	Pro	Leu	Val				
	1650					1655					1660								
Ser	Val	Val	Ser	Glu	Ser	Leu	Thr	Pro	Glu	Arg	Thr	Gln	Leu	Leu	Tyr				
1665					1670					1675					1680				
Leu	Leu	Ala	Val	Ala	Val	Val	Ile	Ile	Leu	Phe	Ile	Ile	Leu	Leu	Gly				
				1685				1690						1695					
Val	Ile	Met	Ala	Lys	Arg	Lys	Arg	Lys	His	Gly	Ser	Leu	Trp	Leu	Pro				
			1700					1705					1710						
Glu	Gly	Phe	Thr	Leu	Arg	Arg	Asp	Ala	Ser	Asn	His	Lys	Arg	Arg	Glu				
		1715					1720					1725							

B

130

Pro Val Gly Gln Asp Ala Val Gly Leu Lys Asn Leu Ser Val Gln Val
1730 1735 1740

Ser Glu Ala Asn Leu Ile Gly Thr Gly Thr Ser Glu His Trp Val Asp
1745 1750 1755 1760

Asp Glu Gly Pro Gln Pro Lys Lys Val Lys Ala Glu Asp Glu Ala Leu
1765 1770 1775

Leu Ser Glu Glu Asp Asp Pro Ile Asp Arg Arg Pro Trp Thr Gln Gln
1780 1785 1790

His Leu Glu Ala Ala Asp Ile Arg Arg Thr Pro Ser Leu Ala Leu Thr
1795 1800 1805

Pro Pro Gln Ala Glu Gln Glu Val Asp Val Leu Asp Val Asn Val Arg
1810 1815 1820

Gly Pro Asp Gly Cys Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly
1825 1830 1835 1840

Ser Ser Asp Leu Ser Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala
1845 1850 1855

Asn Ile Ile Thr Asp Leu Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln
1860 1865 1870

Thr Asp Arg Thr Gly Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser
1875 1880 1885

Arg Ala Asp Ala Ala Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn
1890 1895 1900

Ala Gln Asp Asn Met Gly Arg Cys Pro Leu His Ala Ala Val Ala Ala
1905 1910 1915 1920

Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg Val Thr Asp
1925 1930 1935

Leu Asp Ala Arg Met Asn Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala
1940 1945 1950

Arg Leu Ala Val Glu Gly Met Val Ala Glu Leu Ile Asn Cys Gln Ala
1955 1960 1965

Asp Val Asn Ala Val Asp Asp His Gly Lys Ser Ala Leu His Trp Ala
1970 1975 1980

Ala Ala Val Asn Asn Val Glu Ala Thr Leu Leu Leu Leu Lys Asn Gly
1985 1990 1995 2000

Ala Asn Arg Asp Met Gln Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu
2005 2010 2015

Ala Ala Arg Glu Gly Ser Tyr Glu Ala Ala Lys Ile Leu Leu Asp His
2020 2025 2030

Phe Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp
2035 2040 2045

Val Ala Arg Asp Arg Met His His Asp Ile Val Arg Leu Leu Asp Glu
2050 2055 2060

Tyr Asn Val Thr Pro Ser Pro Pro Gly Thr Val Leu Thr Ser Ala Leu
2065 2070 2075 2080

Ser Pro Val Ile Cys Gly Pro Asn Arg Ser Phe Leu Ser Leu Lys His

B

131

2085					2090					2095					
Thr	Pro	Met	Gly	Lys	Lys	Ser	Arg	Arg	Pro	Ser	Ala	Lys	Ser	Thr	Met
			2100					2105					2110		
Pro	Thr	Ser	Leu	Pro	Asn	Leu	Ala	Lys	Glu	Ala	Lys	Asp	Ala	Lys	Gly
		2115					2120					2125			
Ser	Arg	Arg	Lys	Lys	Ser	Leu	Ser	Glu	Lys	Val	Gln	Leu	Ser	Glu	Ser
	2130					2135					2140				
Ser	Val	Thr	Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	Thr	Tyr
	2145					2150					2155				2160
Val	Ser	Asp	Thr	Thr	Ser	Ser	Pro	Met	Ile	Thr	Ser	Pro	Gly	Ile	Leu
				2165					2170					2175	
Gln	Ala	Ser	Pro	Asn	Pro	Met	Leu	Ala	Thr	Ala	Ala	Pro	Pro	Ala	Pro
			2180					2185					2190		
Val	His	Ala	Gln	His	Ala	Leu	Ser	Phe	Ser	Asn	Leu	His	Glu	Met	Gln
		2195					2200					2205			
Pro	Leu	Ala	His	Gly	Ala	Ser	Thr	Val	Leu	Pro	Ser	Val	Ser	Gln	Leu
	2210					2215					2220				
Leu	Ser	His	His	His	Ile	Val	Ser	Pro	Gly	Ser	Gly	Ser	Ala	Gly	Ser
	2225					2230					2235				2240
Leu	Ser	Arg	Leu	His	Pro	Val	Pro	Val	Pro	Ala	Asp	Trp	Met	Asn	Arg
				2245					2250					2255	
Met	Glu	Val	Asn	Glu	Thr	Gln	Tyr	Asn	Glu	Met	Phe	Gly	Met	Val	Leu
			2260					2265					2270		
Ala	Pro	Ala	Glu	Gly	Thr	His	Pro	Gly	Ile	Ala	Pro	Gln	Ser	Arg	Pro
		2275					2280					2285			
Pro	Glu	Gly	Lys	His	Ile	Thr	Thr	Pro	Arg	Glu	Pro	Leu	Pro	Pro	Ile
	2290					2295					2300				
Val	Thr	Phe	Gln	Leu	Ile	Pro	Lys	Gly	Ser	Ile	Ala	Gln	Pro	Ala	Gly
	2305					2310					2315				2320
Ala	Pro	Gln	Pro	Gln	Ser	Thr	Cys	Pro	Pro	Ala	Val	Ala	Gly	Pro	Leu
				2325					2330					2335	
Pro	Thr	Met	Tyr	Gln	Ile	Pro	Glu	Met	Ala	Arg	Leu	Pro	Ser	Val	Ala
			2340					2345					2350		
Phe	Pro	Thr	Ala	Met	Met	Pro	Gln	Gln	Asp	Gly	Gln	Val	Ala	Gln	Thr
			2355				2360					2365			
Ile	Leu	Pro	Ala	Tyr	His	Pro	Phe	Pro	Ala	Ser	Val	Gly	Lys	Tyr	Pro
	2370					2375					2380				
Thr	Pro	Pro	Ser	Gln	His	Ser	Tyr	Ala	Ser	Ser	Asn	Ala	Ala	Glu	Arg
	2385					2390					2395				2400
Thr	Pro	Ser	His	Ser	Gly	His	Leu	Gln	Gly	Glu	His	Pro	Tyr	Leu	Thr
				2405					2410					2415	
Pro	Ser	Pro	Glu	Ser	Pro	Asp	Gln	Trp	Ser	Ser	Ser	Ser	Pro	His	Ser
			2420					2425					2430		
Ala	Ser	Asp	Trp	Ser	Asp	Val	Thr	Thr	Ser	Pro	Thr	Pro	Gly	Gly	Ala
			2435				2440					2445			

B

132

Gly Gly Gly Gln Arg Gly Pro Gly Thr His Met Ser Glu Pro Pro His
2450 2455 2460

Asn Asn Met Gln Val Tyr Ala
2465 2470

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2556 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Pro Pro Leu Leu Ala Pro Leu Leu Cys Leu Ala Leu Leu Pro Ala
1 5 10 15

Leu Ala Ala Arg Gly Pro Arg Cys Ser Gln Pro Gly Glu Thr Cys Leu
20 25 30

Asn Gly Gly Lys Cys Glu Ala Ala Asn Gly Thr Glu Ala Cys Val Cys
35 40 45

Gly Gly Ala Phe Val Gly Pro Arg Cys Gln Asp Pro Asn Pro Cys Leu
50 55 60

Ser Thr Pro Cys Lys Asn Ala Gly Thr Cys His Val Val Asp Arg Arg
65 70 75 80

Gly Val Ala Asp Tyr Ala Cys Ser Cys Ala Leu Gly Phe Ser Gly Pro
85 90 95

Leu Cys Leu Thr Pro Leu Asp Asn Ala Cys Leu Thr Asn Pro Cys Arg
100 105 110

Asn Gly Gly Thr Cys Asp Leu Leu Thr Leu Thr Glu Tyr Lys Cys Arg
115 120 125

Cys Pro Pro Gly Trp Ser Gly Lys Ser Cys Gln Gln Ala Asp Pro Cys
130 135 140

Ala Ser Asn Pro Cys Ala Asn Gly Gly Gln Cys Leu Pro Phe Glu Ala
145 150 155 160

Ser Tyr Ile Cys His Cys Pro Pro Ser Phe His Gly Pro Thr Cys Arg
165 170 175

Gln Asp Val Asn Glu Cys Gly Gln Lys Pro Arg Leu Cys Arg His Gly
180 185 190

Gly Thr Cys His Asn Glu Val Gly Ser Tyr Arg Cys Val Cys Arg Ala
195 200 205

Thr His Thr Gly Pro Asn Cys Glu Arg Pro Tyr Val Pro Cys Ser Pro
210 215 220

Ser Pro Cys Gln Asn Gly Gly Thr Cys Arg Pro Thr Gly Asp Val Thr
225 230 235 240

His Glu Cys Ala Cys Leu Pro Gly Phe Thr Gly Gln Asn Cys Glu Glu
245 250 255

B

133

Asn Ile Asp Asp Cys Pro Gly Asn Asn Cys Lys Asn Gly Gly Ala Cys
 260 265 270
 Val Asp Gly Val Asn Thr Tyr Asn Cys Pro Cys Pro Pro Glu Trp Thr
 275 280 285
 Gly Gln Tyr Cys Thr Glu Asp Val Asp Glu Cys Gln Leu Met Pro Asn
 290 295 300
 Ala Cys Gln Asn Gly Gly Thr Cys His Asn Thr His Gly Gly Tyr Asn
 305 310 315 320
 Cys Val Cys Val Asn Gly Trp Thr Gly Glu Asp Cys Ser Glu Asn Ile
 325 330 335
 Asp Asp Cys Ala Ser Ala Ala Cys Phe His Gly Ala Thr Cys His Asp
 340 345 350
 Arg Val Ala Ser Phe Tyr Cys Glu Cys Pro His Gly Arg Thr Gly Leu
 355 360 365
 Leu Cys His Leu Asn Asp Ala Cys Ile Ser Asn Pro Cys Asn Glu Gly
 370 375 380
 Ser Asn Cys Asp Thr Asn Pro Val Asn Gly Lys Ala Ile Cys Thr Cys
 385 390 395 400
 Pro Ser Gly Tyr Thr Gly Pro Ala Cys Ser Gln Asp Val Asp Glu Cys
 405 410 415
 Ser Leu Gly Ala Asn Pro Cys Glu His Ala Gly Lys Cys Ile Asn Thr
 420 425 430
 Leu Gly Ser Phe Glu Cys Gln Cys Leu Gln Gly Tyr Thr Gly Pro Arg
 435 440 445
 Cys Glu Ile Asp Val Asn Glu Cys Val Ser Asn Pro Cys Gln Asn Asp
 450 455 460
 Ala Thr Cys Leu Asp Gln Ile Gly Glu Phe Gln Cys Met Cys Met Pro
 465 470 475 480
 Gly Tyr Glu Gly Val His Cys Glu Val Asn Thr Asp Glu Cys Ala Ser
 485 490 495
 Ser Pro Cys Leu His Asn Gly Arg Cys Leu Asp Lys Ile Asn Glu Phe
 500 505 510
 Gln Cys Glu Cys Pro Thr Gly Phe Thr Gly His Leu Cys Gln Tyr Asp
 515 520 525
 Val Asp Glu Cys Ala Ser Thr Pro Cys Lys Asn Gly Ala Lys Cys Leu
 530 535 540
 Asp Gly Pro Asn Thr Tyr Thr Cys Val Cys Thr Glu Gly Tyr Thr Gly
 545 550 555 560
 Thr His Cys Glu Val Asp Ile Asp Glu Cys Asp Pro Asp Pro Cys His
 565 570 575
 Tyr Gly Ser Cys Lys Asp Gly Val Ala Thr Phe Thr Cys Leu Cys Arg
 580 585 590
 Pro Gly Tyr Thr Gly His His Cys Glu Thr Asn Ile Asn Glu Cys Ser
 595 600 605
 Ser Gln Pro Cys Arg Leu Arg Gly Thr Cys Gln Asp Pro Asp Asn Ala

B

134

610	615	620
Tyr 625	Leu Cys Phe Cys Leu 630	Lys Gly Thr Thr Gly 635
Asn 640	Leu Asp Asp Cys Ala Ser Ser Pro Cys 645	Asp Ser Gly Thr Cys Leu 655
Asp 660	Lys Ile Asp Gly Tyr Glu Cys Ala 665	Cys Glu Pro Gly Tyr Thr Gly 670
Ser 675	Met Cys Asn Ser Asn Ile Asp 680	Glu Cys Ala Gly Asn Pro Cys His 685
Asn 690	Gly Gly Thr Cys Glu Asp Gly Ile Asn Gly 695	Phe Thr Cys Arg Cys 700
Pro 705	Glu Gly Tyr His Asp Pro Thr Cys Leu 710	Ser Glu Val Asn Glu Cys 715
Asn 720	Ser Asn Pro Cys Val His Gly Ala Cys 725	Arg Asp Ser Leu Asn Gly 735
Tyr 740	Lys Cys Asp Cys Asp Pro Gly Trp 745	Ser Gly Thr Asn Cys Asp Ile 750
Asn 755	Asn Asn Glu Cys Glu Ser Asn Pro Cys 760	Val Asn Gly Gly Thr Cys 765
Lys 770	Asp Met Thr Ser Gly Ile Val Cys Thr 775	Cys Arg Glu Gly Phe Ser 780
Gly 785	Pro Asn Cys Gln Thr Asn Ile Asn Glu 790	Cys Ala Ser Asn Pro Cys 795
Leu 805	Asn Lys Gly Thr Cys Ile Asp Asp Val 810	Ala Gly Tyr Lys Cys Asn 815
Cys 820	Leu Leu Pro Tyr Thr Gly Ala Thr 825	Cys Glu Val Val Leu Ala Pro 830
Cys 835	Ala Pro Ser Pro Cys Arg Asn Gly 840	Gly Glu Cys Arg Gln Ser Glu 845
Asp 850	Tyr Glu Ser Phe Ser Cys Val Cys Pro 855	Thr Ala Gly Ala Lys Gly 860
Gln 865	Thr Cys Glu Val Asp Ile Asn Glu 870	Cys Val Leu Ser Pro Cys Arg 875
His 885	Gly Ala Ser Cys Gln Asn Thr His Gly 890	Gly Tyr Arg Cys His Cys 895
Gln 900	Ala Gly Tyr Ser Gly Arg Asn Cys 905	Glu Thr Asp Ile Asp Asp Cys 910
Arg 915	Pro Asn Pro Cys His Asn Gly 920	Gly Ser Cys Thr Asp Gly Ile Asn 925
Thr 930	Ala Phe Cys Asp Cys Leu Pro Gly 935	Phe Arg Gly Thr Phe Cys Glu 940
Glu 945	Asp Ile Asn Glu Cys Ala Ser Asp Pro 950	Cys Arg Asn Gly Ala Asn 955
Cys 965	Thr Asp Cys Val Asp Ser Tyr Thr 970	Cys Thr Cys Pro Ala Gly Phe 975

B

135

Ser Gly Ile His Cys Glu Asn Asn Thr Pro Asp Cys Thr Glu Ser Ser
980 985 990

Cys Phe Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser Phe Thr Cys
995 1000 1005

Leu Cys Pro Pro Gly Phe Thr Gly Ser Tyr Cys Gln His Val Val Asn
1010 1015 1020

Glu Cys Asp Ser Arg Pro Cys Leu Leu Gly Gly Thr Cys Gln Asp Gly
1025 1030 1035 1040

Arg Gly Leu His Arg Cys Thr Cys Pro Gln Gly Tyr Thr Gly Pro Asn
1045 1050 1055

Cys Gln Asn Leu Val His Trp Cys Asp Ser Ser Pro Cys Lys Asn Gly
1060 1065 1070

Gly Lys Cys Trp Gln Thr His Thr Gln Tyr Arg Cys Glu Cys Pro Ser
1075 1080 1085

Gly Trp Thr Gly Leu Tyr Cys Asp Val Pro Ser Val Ser Cys Glu Val
1090 1095 1100

Ala Ala Gln Arg Gln Gly Val Asp Val Ala Arg Leu Cys Gln His Gly
1105 1110 1115 1120

Gly Leu Cys Val Asp Ala Gly Asn Thr His His Cys Arg Cys Gln Ala
1125 1130 1135

Gly Tyr Thr Gly Ser Tyr Cys Glu Asp Leu Val Asp Glu Cys Ser Pro
1140 1145 1150

Ser Pro Cys Gln Asn Gly Ala Thr Cys Thr Asp Tyr Leu Gly Gly Tyr
1155 1160 1165

Ser Cys Lys Cys Val Ala Gly Tyr His Gly Val Asn Cys Ser Glu Glu
1170 1175 1180

Ile Asp Glu Cys Leu Ser His Pro Cys Gln Asn Gly Gly Thr Cys Leu
1185 1190 1195 1200

Asp Leu Pro Asn Thr Tyr Lys Cys Ser Cys Pro Arg Gly Thr Gln Gly
1205 1210 1215

Val His Cys Glu Ile Asn Val Asp Asp Cys Asn Pro Pro Val Asp Pro
1220 1225 1230

Val Ser Arg Ser Pro Lys Cys Phe Asn Asn Gly Thr Cys Val Asp Gln
1235 1240 1245

Val Gly Gly Tyr Ser Cys Thr Cys Pro Pro Gly Phe Val Gly Glu Arg
1250 1255 1260

Cys Glu Gly Asp Val Asn Glu Cys Leu Ser Asn Pro Cys Asp Ala Arg
1265 1270 1275 1280

Gly Thr Gln Asn Cys Val Gln Arg Val Asn Asp Phe His Cys Glu Cys
1285 1290 1295

Arg Ala Gly His Thr Gly Arg Arg Cys Glu Ser Val Ile Asn Gly Cys
1300 1305 1310

Lys Gly Lys Pro Cys Lys Asn Gly Gly Thr Cys Ala Val Ala Ser Asn
1315 1320 1325

Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala

1330	1335	1340
Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 1345 1350 1355 1360		
Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu 1365 1370 1375		
Gly Pro Phe Thr Gly Pro Glu Cys Gln Phe Pro Ala Ser Ser Pro Cys 1380 1385 1390		
Leu Gly Gly Asn Pro Cys Tyr Asn Gln Gly Thr Cys Glu Pro Thr Ser 1395 1400 1405		
Glu Ser Pro Phe Tyr Arg Cys Leu Cys Pro Ala Lys Phe Asn Gly Leu 1410 1415 1420		
Leu Cys His Ile Leu Asp Tyr Ser Phe Gly Gly Gly Ala Gly Arg Asp 1425 1430 1435 1440		
Ile Pro Pro Pro Leu Ile Glu Glu Ala Cys Glu Leu Pro Glu Cys Gln 1445 1450 1455		
Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn His Ala 1460 1465 1470		
Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp Pro Trp 1475 1480 1485		
Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser Asp Gly 1490 1495 1500		
His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp Gly Phe 1505 1510 1515 1520		
Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp Gln Tyr 1525 1530 1535		
Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys Asn Ser 1540 1545 1550		
Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val Pro Glu 1555 1560 1565		
Arg Leu Ala Ala Gly Thr Leu Val Val Val Val Leu Met Pro Pro Glu 1570 1575 1580		
Gln Leu Arg Asn Ser Ser Phe His Phe Leu Arg Glu Leu Ser Arg Val 1585 1590 1595 1600		
Leu His Thr Asn Val Val Phe Lys Arg Asp Ala His Gly Gln Gln Met 1605 1610 1615		
Ile Phe Pro Tyr Tyr Gly Arg Glu Glu Glu Leu Arg Lys His Pro Ile 1620 1625 1630		
Lys Arg Ala Ala Glu Gly Trp Ala Ala Pro Asp Ala Leu Leu Gly Gln 1635 1640 1645		
Val Lys Ala Ser Leu Leu Pro Gly Gly Ser Glu Gly Gly Arg Arg Arg 1650 1655 1660		
Arg Glu Leu Asp Pro Met Asp Val Arg Gly Ser Ile Val Tyr Leu Glu 1665 1670 1675 1680		
Ile Asp Asn Arg Gln Cys Val Gln Ala Ser Ser Gln Cys Phe Gln Ser 1685 1690 1695		

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Ala Thr Asp Val Ala Ala Phe Leu Gly Ala Leu Ala Ser Leu Gly Ser
1700 1705 1710

Leu Asn Ile Pro Tyr Lys Ile Glu Ala Val Gln Ser Glu Thr Val Glu
1715 1720 1725

Pro Pro Pro Pro Ala Gln Leu His Phe Met Tyr Val Ala Ala Ala Ala
1730 1735 1740

Phe Val Leu Leu Phe Phe Val Gly Cys Gly Val Leu Leu Ser Arg Lys
1745 1750 1755 1760

Arg Arg Arg Gln His Gly Gln Leu Trp Phe Pro Glu Gly Phe Lys Val
1765 1770 1775

Ser Glu Ala Ser Lys Lys Lys Arg Arg Glu Glu Leu Gly Glu Asp Ser
1780 1785 1790

Val Gly Leu Lys Pro Leu Lys Asn Ala Ser Asp Gly Ala Leu Met Asp
1795 1800 1805

Asp Asn Gln Asn Glu Trp Gly Asp Glu Asp Leu Glu Thr Lys Lys Phe
1810 1815 1820

Arg Phe Glu Glu Pro Val Val Leu Pro Asp Leu Asp Asp Gln Thr Asp
1825 1830 1835 1840

His Arg Gln Trp Thr Gln Gln His Leu Asp Ala Ala Asp Leu Arg Met
1845 1850 1855

Ser Ala Met Ala Pro Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys
1860 1865 1870

Met Asp Val Asn Val Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile
1875 1880 1885

Ala Ser Cys Ser Gly Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu
1890 1895 1900

Glu Asp Ala Pro Ala Val Ile Ser Asp Phe Ile Tyr Gln Gly Ala Ser
1905 1910 1915 1920

Leu His Asn Gln Thr Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala
1925 1930 1935

Ala Arg Tyr Ser Arg Ser Asp Ala Ala Lys Arg Leu Leu Glu Ala Ser
1940 1945 1950

Ala Asp Ala Asn Ile Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala
1955 1960 1965

Ala Val Ser Ala Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn
1970 1975 1980

Arg Ala Thr Asp Leu Asp Ala Arg Met His Asp Gly Thr Thr Pro Leu
1985 1990 1995 2000

Ile Leu Ala Ala Arg Leu Ala Val Glu Gly Met Leu Glu Asp Leu Ile
2005 2010 2015

Asn Ser His Ala Asp Val Asn Ala Val Asp Asp Leu Gly Lys Ser Ala
2020 2025 2030

Leu His Trp Ala Ala Ala Val Asn Asn Val Asp Ala Ala Val Val Leu
2035 2040 2045

Leu Lys Asn Gly Ala Asn Lys Asp Met Gln Asn Asn Arg Glu Glu Thr

B

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2050	2055	2060
Pro Leu Phe Leu Ala Ala Arg Glu Gly Ser Tyr Glu Thr Ala Lys Val 2065	2070	2075 2080
Leu Leu Asp His Phe Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg 2085	2090	2095
Leu Pro Arg Asp Ile Ala Gln Glu Arg Met His His Asp Ile Val Arg 2100	2105	2110
Leu Leu Asp Glu Tyr Asn Leu Val Arg Ser Pro Gln Leu His Gly Ala 2115	2120	2125
Pro Leu Gly Gly Thr Pro Thr Leu Ser Pro Pro Leu Cys Ser Pro Asn 2130	2135	2140
Gly Tyr Leu Gly Ser Leu Lys Pro Gly Val Gln Gly Lys Lys Val Arg 2145	2150	2155 2160
Lys Pro Ser Ser Lys Gly Leu Ala Cys Gly Ser Lys Glu Ala Lys Asp 2165	2170	2175
Leu Lys Ala Arg Arg Lys Lys Ser Gln Asp Gly Lys Gly Cys Leu Leu 2180	2185	2190
Asp Ser Ser Gly Met Leu Ser Pro Val Asp Ser Leu Glu Ser Pro His 2195	2200	2205
Gly Tyr Leu Ser Asp Val Ala Ser Pro Pro Leu Leu Pro Ser Pro Phe 2210	2215	2220
Gln Gln Ser Pro Ser Val Pro Leu Asn His Leu Pro Gly Met Pro Asp 2225	2230	2235 2240
Thr His Leu Gly Ile Gly His Leu Asn Val Ala Ala Lys Pro Glu Met 2245	2250	2255
Ala Ala Leu Gly Gly Gly Gly Arg Leu Ala Phe Glu Thr Gly Pro Pro 2260	2265	2270
Arg Leu Ser His Leu Pro Val Ala Ser Gly Thr Ser Thr Val Leu Gly 2275	2280	2285
Ser Ser Ser Gly Gly Ala Leu Asn Phe Thr Val Gly Gly Ser Thr Ser 2290	2295	2300
Leu Asn Gly Gln Cys Glu Trp Leu Ser Arg Leu Gln Ser Gly Met Val 2305	2310	2315 2320
Pro Asn Gln Tyr Asn Pro Leu Arg Gly Ser Val Ala Pro Gly Pro Leu 2325	2330	2335
Ser Thr Gln Ala Pro Ser Leu Gln His Gly Met Val Gly Pro Leu His 2340	2345	2350
Ser Ser Leu Ala Ala Ser Ala Leu Ser Gln Met Met Ser Tyr Gln Gly 2355	2360	2365
Leu Pro Ser Thr Arg Leu Ala Thr Gln Pro His Leu Val Gln Thr Gln 2370	2375	2380
Gln Val Gln Pro Gln Asn Leu Gln Met Gln Gln Gln Asn Leu Gln Pro 2385	2390	2395 2400
Ala Asn Ile Gln Gln Gln Gln Ser Leu Gln Pro Pro Pro Pro Pro Pro 2405	2410	2415

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Gln Pro His Leu Gly Val Ser Ser Ala Ala Ser Gly His Leu Gly Arg
2420 2425 2430

Ser Phe Leu Ser Gly Glu Pro Ser Gln Ala Asp Val Gln Pro Leu Gly
2435 2440 2445

Pro Ser Ser Leu Ala Val His Thr Ile Leu Pro Gln Glu Ser Pro Ala
2450 2455 2460

Leu Pro Thr Ser Leu Pro Ser Ser Leu Val Pro Pro Val Thr Ala Ala
2465 2470 2475 2480

Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro Val Glu
2485 2490 2495

Asn Thr Pro Ser His Gln Leu Gln Val Pro Glu His Pro Phe Leu Thr
2500 2505 2510

Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser
2515 2520 2525

Asn Val Ser Asp Trp Ser Glu Gly Val Ser Ser Pro Pro Thr Ser Met
2530 2535 2540

Gln Ser Gln Ile Ala Arg Ile Pro Glu Ala Phe Lys
2545 2550 2555

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 10..7419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCCG CCC GCC CTG CGC CCC GCT CTG CTG TGG GCG CTG CTG GCG	48
Pro Ala Leu Arg Pro Ala Leu Leu Trp Ala Leu Leu Ala	
1 5 10	
CTC TGG CTG TGC TGC GCG GCC CCC GCG CAT GCA TTG CAG TGT CGA GAT	96
Leu Trp Leu Cys Cys Ala Ala Pro Ala His Ala Leu Gln Cys Arg Asp	
15 20 25	
GGC TAT GAA CCC TGT GTA AAT GAA GGA ATG TGT GTT ACC TAC CAC AAT	144
Gly Tyr Glu Pro Cys Val Asn Glu Gly Met Cys Val Thr Tyr His Asn	
30 35 40 45	
GGC ACA GGA TAC TGC AAA TGT CCA GAA GGC TTC TTG GGG GAA TAT TGT	192
Gly Thr Gly Tyr Cys Lys Cys Pro Glu Gly Phe Leu Gly Glu Tyr Cys	
50 55 60	
CAA CAT CGA GAC CCC TGT GAG AAG AAC CGC TGC CAG AAT GGT GGG ACT	240
Gln His Arg Asp Pro Cys Glu Lys Asn Arg Cys Gln Asn Gly Gly Thr	
65 70 75	
TGT GTG GCC CAG GCC ATG CTG GGG AAA GCC ACG TGC CGA TGT GCC TCA	288
Cys Val Ala Gln Ala Met Leu Gly Lys Ala Thr Cys Arg Cys Ala Ser	

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80						85					90					
GGG Gly	TTT Phe 95	ACA Thr	GGA Gly	GAG Glu	GAC Asp	TGC Cys 100	CAG Gln	TAC Tyr	TCA Ser	ACA Thr	TCT Ser 105	CAT His	CCA Pro	TGC Cys	TTT Phe	336
GTG Val 110	TCT Ser	CGA Arg	CCC Pro	TGC Cys	CTG Leu 115	AAT Asn	GGC Gly	GGC Gly	ACA Thr	TGC Cys 120	CAT His	ATG Met	CTC Leu	AGC Ser	CGG Arg 125	384
GAT Asp	ACC Thr	TAT Tyr	GAG Glu	TGC Cys 130	ACC Thr	TGT Cys	CAA Gln	GTC Val	GGG Gly 135	TTT Phe	ACA Thr	GGT Gly	AAG Lys	GAG Glu 140	TGC Cys	432
CAA Gln	TGG Trp	ACG Thr	GAT Asp 145	GCC Ala	TGC Cys	CTG Leu	TCT Ser	CAT His 150	CCC Pro	TGT Cys	GCA Ala	AAT Asn	GGA Gly 155	AGT Ser	ACC Thr	480
TGT Cys	ACC Thr	ACT Thr 160	GTG Val	GCC Ala	AAC Asn	CAG Gln	TTC Phe 165	TCC Ser	TGC Cys	AAA Lys	TGC Cys	CTC Leu 170	ACA Thr	GGC Gly	TTC Phe	528
ACA Thr	GGG Gly 175	CAG Gln	AAA Lys	TGT Cys	GAG Glu	ACT Thr 180	GAT Asp	GTC Val	AAT Asn	GAG Glu	TGT Cys 185	GAC Asp	ATT Ile	CCA Pro	GGA Gly	576
CAC His 190	TGC Cys	CAG Gln	CAT His	GGT Gly	GGC Gly 195	ACC Thr	TGC Cys	CTC Leu	AAC Asn	CTG Leu 200	CCT Pro	GGT Gly	TCC Ser	TAC Tyr	CAG Gln 205	624
TGC Cys	CAG Gln	TGC Cys	CCT Pro	CAG Gln 210	GGC Gly	TTC Phe	ACA Thr	GGC Gly	CAG Gln 215	TAC Tyr	TGT Cys	GAC Asp	AGC Ser	CTG Leu 220	TAT Tyr	672
GTG Val	CCC Pro	TGT Cys	GCA Ala 225	CCC Pro	TCA Ser	CCT Pro	TGT Cys	GTC Val 230	AAT Asn	GGA Gly	GGC Gly	ACC Thr	TGT Cys 235	CGG Arg	CAG Gln	720
ACT Thr	GGT Gly	GAC Asp 240	TTC Phe	ACT Thr	TTT Phe	GAG Glu	TGC Cys 245	AAC Asn	TGC Cys	CTT Leu	CCA Pro	GGT Gly 250	TTT Phe	GAA Glu	GGG Gly	768
AGC Ser	ACC Thr 255	TGT Cys	GAG Glu	AGG Arg	AAT Asn	ATT Ile 260	GAT Asp	GAC Asp	TGC Cys	CCT Pro	AAC Asn 265	CAC His	AGG Arg	TGT Cys	CAG Gln	816
AAT Asn 270	GGA Gly	GGG Gly	GTT Val	TGT Cys	GTG Val 275	GAT Asp	GGG Gly	GTC Val	AAC Asn	ACT Thr 280	TAC Tyr	AAC Asn	TGC Cys	CGC Arg	TGT Cys 285	864
CCC Pro	CCA Pro	CAA Gln	TGG Trp	ACA Thr 290	GGA Gly	CAG Gln	TTC Phe	TGC Cys	ACA Thr 295	GAG Glu	GAT Asp	GTG Val	GAT Asp	GAA Glu 300	TGC Cys	912
CTG Leu	CTG Leu	CAG Gln	CCC Pro 305	AAT Asn	GCC Ala	TGT Cys	CAA Gln	AAT Asn 310	GGG Gly	GGC Gly	ACC Thr	TGT Cys	GCC Ala 315	AAC Asn	CGC Arg	960
AAT Asn	GGA Gly	GGC Gly 320	TAT Tyr	GGC Gly	TGT Cys	GTA Val	TGT Cys 325	GTC Val	AAC Asn	GGC Gly	TGG Trp 330	AGT Ser 335	GGA Gly	GAT Asp	GAC Asp	1008
TGC Cys	AGT Ser 335	GAG Glu	AAC Asn	ATT Ile	GAT Asp	GAT Asp 340	TGT Cys	GCC Ala	TTC Phe	GCC Ala	TCC Ser 345	TGT Cys	ACT Thr	CCA Pro	GGC Gly	1056
TCC Cys	ACC Thr	TGC Cys	ATC Thr	GAC Glu	CGT Gln	GTG Gln	GCC Gln	TCC Ser	TTC Phe	TCT Leu	TGC Cys	ATG Met	TGC Cys	CCA Pro	GAG Glu	1104

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Ser 350	Thr	Cys	Ile	Asp	Arg 355	Val	Ala	Ser	Phe	Ser 360	Cys	Met	Cys	Pro	Glu 365	
GGG Gly	AAG Lys	GCA Ala	GGT Gly	CTC Leu 370	CTG Leu	TGT Cys	CAT His	CTG Leu	GAT Asp 375	GAT Asp	GCA Ala	TGC Cys	ATC Ile	AGC Ser 380	AAT Asn	1152
CCT Pro	TGC Cys	CAC His	AAG Lys 385	GGG Gly	GCA Ala	CTG Leu	TGT Cys	GAC Asp 390	ACC Thr	AAC Asn	CCC Pro	CTA Leu	AAT Asn 395	GGG Gly	CAA Gln	1200
TAT Tyr	ATT Ile	TGC Cys 400	ACC Thr	TGC Cys	CCA Pro	CAA Gln	GGC Gly 405	TAC Tyr	AAA Lys	GGG Gly	GCT Ala	GAC Asp 410	TGC Cys	ACA Thr	GAA Glu	1248
GAT Asp	GTG Val 415	GAT Asp	GAA Glu	TGT Cys	GCC Ala	ATG Met 420	GCC Ala	AAT Asn	AGC Ser	AAT Asn	CCT Pro 425	TGT Cys	GAG Glu	CAT His	GCA Ala	1296
GGA Gly 430	AAA Lys	TGT Cys	GTG Val	AAC Asn	ACG Thr 435	GAT Asp	GGC Gly	GCC Ala	TTC Phe	CAC His 440	TGT Cys	GAG Glu	TGT Cys	CTG Leu	AAG Lys 445	1344
GGT Gly	TAT Tyr	GCA Ala	GGA Gly	CCT Pro 450	CGT Arg	TGT Cys	GAG Glu	ATG Met	GAC Asp 455	ATC Ile	AAT Asn	GAG Glu	TGC Cys	CAT His 460	TCA Ser	1392
GAC Asp	CCC Pro	TGC Cys	CAG Gln 465	AAT Asn	GAT Asp	GCT Ala	ACC Thr	TGT Cys 470	CTG Leu	GAT Asp	AAG Lys	ATT Ile	GGA Gly 475	GGC Gly	TTC Phe	1440
ACA Thr	TGT Cys	CTG Leu 480	TGC Cys	ATG Met	CCA Pro	GGT Gly	TTC Phe 485	AAA Lys	GGT Gly	GTG Val	CAT His	TGT Cys 490	GAA Glu	TTA Leu	GAA Glu	1488
ATA Ile	AAT Asn 495	GAA Glu	TGT Cys	CAG Gln	AGC Ser	AAC Asn 500	CCT Pro	TGT Cys	GTG Val	AAC Asn 505	AAT Asn	GGG Gly	CAG Gln	TGT Cys	GTG Val	1536
GAT Asp 510	AAA Lys	GTC Val	AAT Asn	CGT Arg	TTC Phe 515	CAG Gln	TGC Cys	CTG Leu	TGT Cys	CCT Pro 520	CCT Pro	GGT Gly	TTC Phe	ACT Thr	GGG Gly 525	1584
CCA Pro	GTT Val	TGC Cys	CAG Gln	ATT Ile 530	GAT Asp	ATT Ile	GAT Asp	GAC Asp	TGT Cys 535	TCC Ser	AGT Ser	ACT Thr	CCG Pro	TGT Cys 540	CTG Leu	1632
AAT Asn	GGG Gly	GCA Ala	AAG Lys 545	TGT Cys	ATC Ile	GAT Asp	CAC His	CCG Pro 550	AAT Asn	GGC Gly	TAT Tyr	GAA Glu	TGC Cys 555	CAG Gln	TGT Cys	1680
GCC Ala	ACA Thr	GGT Gly 560	TTC Phe	ACT Thr	GGT Gly	GTG Val	TTG Leu 565	TGT Cys	GAG Glu	GAG Glu	AAC Asn	ATT Ile 570	GAC Asp	AAC Asn	TGT Cys	1728
GAC Asp	CCC Pro 575	GAT Asp	CCT Pro	TGC Cys	CAC His	CAT His 580	GGT Gly	CAG Gln	TGT Cys	CAG Gln	GAT Asp 585	GGT Gly	ATT Ile	GAT Asp	TCC Ser	1776
TAC Tyr 590	ACC Thr	TGC Cys	ATC Ile	TGC Cys	AAT Asn 595	CCC Pro	GGG Gly	TAC Tyr	ATG Met	GGC Gly 600	GCC Ala	ATC Ile	TGC Cys	AGT Ser	GAC Asp 605	1824
CAG Gln	ATT Ile	GAT Asp	GAA Glu	TGT Cys 610	TAC Tyr	AGC Ser	AGC Ser	CCT Pro	TGC Cys 615	CTG Leu	AAC Asn	GAT Asp	GGT Gly	CGC Arg 620	TGC Cys	1872

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ATT Ile	GAC Asp	CTG Leu	GTC Val 625	AAT Asn	GGC Gly	TAC Tyr	CAG Gln	TGC Cys 630	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GGC Gly 635	ACG Thr	TCA Ser	1920
GGG Gly	GTT Val	AAT Asn 640	TGT Cys	GAA Glu	ATT Ile	AAT Asn	TTT Phe 645	GAT Asp	GAC Asp	TGT Cys	GCA Ala	AGT Ser 650	AAC Asn	CCT Pro	TGT Cys	1968
ATC Ile	CAT His 655	GGA Gly	ATC Ile	TGT Cys	ATG Met	GAT Asp 660	GGC Gly	ATT Ile	AAT Asn	CGC Arg	TAC Tyr 665	AGT Ser	TGT Cys	GTC Val	TGC Cys	2016
TCA Ser 670	CCA Pro	GGA Gly	TTC Phe	ACA Thr	GGG Gly 675	CAG Gln	AGA Arg	TGT Cys	AAC Asn	ATT Ile 680	GAC Asp	ATT Ile	GAT Asp	GAG Glu	TGT Cys 685	2064
GCC Ala	TCC Ser	AAT Asn	CCC Pro	TGT Cys 690	CGC Arg	AAG Lys	GGT Gly	GCA Ala	ACA Thr 695	TGT Cys	ATC Ile	AAC Asn	GGT Gly	GTG Val 700	AAT Asn	2112
GGT Gly	TTC Phe	CGC Arg 705	TGT Cys	ATA Ile	TGC Cys	CCC Pro	GAG Glu 710	GGA Gly	CCC Pro	CAT His	CAC His	CCC Pro	AGC Ser 715	TGC Cys	TAC Tyr	2160
TCA Ser	CAG Gln 720	GTG Val	AAC Asn	GAA Glu	TGC Cys	CTG Leu 725	AGC Ser	AAT Asn	CCC Pro	TGC Cys	ATC Ile	CAT His 730	GGA Gly	AAC Asn	TGT Cys	2208
B ACT Thr	GGA Gly 735	GGT Gly	CTC Leu	AGT Ser	GGA Gly	TAT Tyr 740	AAG Lys	TGT Cys	CTC Leu	TGT Cys	GAT Asp 745	GCA Ala	GGC Gly	TGG Trp	GTT Val	2256
GGC Gly 750	ATC Ile	AAC Asn	TGT Cys	GAA Glu	GTG Val 755	GAC Asp	AAA Lys	AAT Asn	GAA Glu	TGC Cys 760	CTT Leu	TCG Ser	AAT Asn	CCA Pro	TGC Cys 765	2304
CAG Gln	AAT Asn	GGA Gly	GGA Gly	ACT Thr 770	TGT Cys	GAC Asp	AAT Asn	CTG Leu	GTG Val 775	AAT Asn	GGA Gly	TAC Tyr	AGG Arg	TGT Cys 780	ACT Thr	2352
TGC Cys	AAG Lys	AAG Lys	GGC Gly 785	TTT Phe	AAA Lys	GGC Gly	TAT Tyr	AAC Asn 790	TGC Cys	CAG Gln	GTG Val	AAT Asn	ATT Ile 795	GAT Asp	GAA Glu	2400
TGT Cys	GCC Ala	TCA Ser 800	AAT Asn	CCA Pro	TGC Cys	CTG Leu	AAC Asn 805	CAA Gln	GGA Gly	ACC Thr	TGC Cys	TTT Phe 810	GAT Asp	GAC Asp	ATA Ile	2448
AGT Ser	GGC Gly 815	TAC Tyr	ACT Thr	TGC Cys	CAC His	TGT Cys 820	GTG Val	CTG Leu	CCA Pro	TAC Tyr	ACA Thr 825	GGC Gly	AAG Lys	AAT Asn	TGT Cys	2496
CAG Gln 830	ACA Thr	GTA Val	TTG Leu	GCT Ala	CCC Pro 835	TGT Cys	TCC Ser	CCA Pro	AAC Asn	CCT Pro 840	TGT Cys	GAG Glu	AAT Asn	GCT Ala	GCT Ala 845	2544
GTT Val	TGC Cys	AAA Lys	GAG Glu	TCA Ser 850	CCA Pro	AAT Asn	TTT Phe	GAG Glu	AGT Ser 855	TAT Tyr	ACT Thr	TGC Cys	TTG Leu	TGT Cys 860	GCT Ala	2592
CCT Pro	GGC Gly	TGG Trp	CAA Gln 865	GGT Gly	CAG Gln	CGG Arg	TGT Cys	ACC Thr 870	ATT Ile	GAC Asp	ATT Ile	GAC Asp	GAG Glu 875	TGT Cys	ATC Ile	2640
TCC Ser	AAG Lys	CCC Pro 880	TGC Cys	ATG Met	AAC Asn	CAT His	GGT Gly 885	CTC Leu	TGC Cys	CAT His	AAC Asn	ACC Thr 890	CAG Gln	GGC Gly	AGC Ser	2688

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TAC Tyr	ATG Met	TGT Cys	GAA Glu	TGT Cys	CCA Pro	CCA Pro	GGC Gly	TTC Phe	AGT Ser	GGT Gly	ATG Met	GAC Asp	TGT Cys	GAG Glu	GAG Glu	2736
895						900					905					
GAC Asp	ATT Ile	GAT Asp	GAC Asp	TGC Cys	CTT Leu	GCC Ala	AAT Asn	CCT Pro	TGC Cys	CAG Gln	AAT Asn	GGA Gly	GGT Gly	TCC Ser	TGT Cys	2784
910					915					920					925	
ATG Met	GAT Asp	GGA Gly	GTG Val	AAT Asn	ACT Thr	TTC Phe	TCC Ser	TGC Cys	CTC Leu	TGC Cys	CTT Leu	CCG Pro	GGT Gly	TTC Phe	ACT Thr	2832
				930					935					940		
GGG Gly	GAT Asp	AAG Lys	TGC Cys	CAG Gln	ACA Thr	GAC Asp	ATG Met	AAT Asn	GAG Glu	TGT Cys	CTG Leu	AGT Ser	GAA Glu	CCC Pro	TGT Cys	2880
			945					950					955			
AAG Lys	AAT Asn	GGA Gly	GGG Gly	ACC Thr	TGC Cys	TCT Ser	GAC Asp	TAC Tyr	GTC Val	AAC Asn	AGT Ser	TAC Tyr	ACT Thr	TGC Cys	AAG Lys	2928
		960					965					970				
TGC Cys	CAG Gln	GCA Ala	GGA Gly	TTT Phe	GAT Asp	GGA Gly	GTC Val	CAT His	TGT Cys	GAG Glu	AAC Asn	AAC Asn	ATC Ile	AAT Asn	GAG Glu	2976
	975					980					985					
TGC Cys	ACT Thr	GAG Glu	AGC Ser	TCC Ser	TGT Cys	TTC Phe	AAT Asn	GGT Gly	GGC Gly	ACA Thr	TGT Cys	GTT Val	GAT Asp	GGG Gly	ATT Ile	3024
990					995					1000					1005	
AAC Asn	TCC Ser	TTC Phe	TCT Ser	TGC Cys	TTG Leu	TGC Cys	CCT Pro	GTG Val	GGT Gly	TTC Phe	ACT Thr	GGA Gly	TCC Ser	TTC Phe	TGC Cys	3072
				1010				1015						1020		
CTC Leu	CAT His	GAG Glu	ATC Ile	AAT Asn	GAA Glu	TGC Cys	AGC Ser	TCT Ser	CAT His	CCA Pro	TGC Cys	CTG Leu	AAT Asn	GAG Glu	GGA Gly	3120
			1025					1030					1035			
ACG Thr	TGT Cys	GTT Val	GAT Asp	GGC Gly	CTG Leu	GGT Gly	ACC Thr	TAC Tyr	CGC Arg	TGC Cys	AGC Ser	TGC Cys	CCC Pro	CTG Leu	GGC Gly	3168
		1040				1045						1050				
TAC Tyr	ACT Thr	GGG Gly	AAA Lys	AAC Asn	TGT Cys	CAG Gln	ACC Thr	CTG Leu	GTG Val	AAT Asn	CTC Leu	TGC Cys	AGT Ser	CGG Arg	TCT Ser	3216
	1055					1060					1065					
CCA Pro	TGT Cys	AAA Lys	AAC Asn	AAA Lys	GGT Gly	ACT Thr	TGT Cys	GTT Val	CAG Gln	AAA Lys	AAA Lys	GCA Ala	GAG Glu	TCC Ser	CAG Gln	3264
1070					1075				1080						1085	
TGC Cys	CTA Leu	TGT Cys	CCA Pro	TCT Ser	GGA Gly	TGG Trp	GCT Ala	GGT Gly	GCC Ala	TAT Tyr	TGT Cys	GAC Asp	GTG Val	CCC Pro	AAT Asn	3312
				1090				1095					1100			
GTC Val	TCT Ser	TGT Cys	GAC Asp	ATA Ile	GCA Ala	GCC Ala	TCC Ser	AGG Arg	AGA Arg	GGT Gly	GTG Val	CTT Leu	GTT Val	GAA Glu	CAC His	3360
			1105					1110					1115			
TTG Leu	TGC Cys	CAG Gln	CAC His	TCA Ser	GGT Gly	GTC Val	TGC Cys	ATC Ile	AAT Asn	GCT Ala	GGC Gly	AAC Asn	ACG Thr	CAT His	TAC Tyr	3408
		1120				1125						1130				
TGT Cys	CAG Gln	TGC Cys	CCC Pro	CTG Leu	GGC Gly	TAT Tyr	ACT Thr	GGG Gly	AGC Ser	TAC Tyr	TGT Cys	GAG Glu	GAG Glu	CAA Gln	CTC Leu	3456
	1135					1140					1145					
GAT Asp	GAG Glu	TGT Cys	GCG Ala	TCC Ser	AAC Asn	CCC Pro	TGC Cys	CAG Gln	CAC His	GGG Gly	GCA Ala	ACA Thr	TGC Cys	AGT Ser	GAC Asp	3504
1150					1155					1160					1165	

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TTC	ATT	GGT	GGA	TAC	AGA	TGC	GAG	TGT	GTC	CCA	GGC	TAT	CAG	GGT	GTC	3552
Phe	Ile	Gly	Gly	Tyr	Arg	Cys	Glu	Cys	Val	Pro	Gly	Tyr	Gln	Gly	Val	
				1170					1175					1180		
AAC	TGT	GAG	TAT	GAA	GTG	GAT	GAG	TGC	CAG	AAT	CAG	CCC	TGC	CAG	AAT	3600
Asn	Cys	Glu	Tyr	Glu	Val	Asp	Glu	Cys	Gln	Asn	Gln	Pro	Cys	Gln	Asn	
			1185					1190					1195			
GGA	GGC	ACC	TGT	ATT	GAC	CTT	GTG	AAC	CAT	TTC	AAG	TGC	TCT	TGC	CCA	3648
Gly	Gly	Thr	Cys	Ile	Asp	Leu	Val	Asn	His	Phe	Lys	Cys	Ser	Cys	Pro	
		1200					1205					1210				
CCA	GGC	ACT	CGG	GGC	CTA	CTC	TGT	GAA	GAG	AAC	ATT	GAT	GAC	TGT	GCC	3696
Pro	Gly	Thr	Arg	Gly	Leu	Leu	Cys	Glu	Glu	Asn	Ile	Asp	Asp	Cys	Ala	
	1215					1220					1225					
CGG	GGT	CCC	CAT	TGC	CTT	AAT	GGT	GGT	CAG	TGC	ATG	GAT	AGG	ATT	GGA	3744
Arg	Gly	Pro	His	Cys	Leu	Asn	Gly	Gly	Gln	Cys	Met	Asp	Arg	Ile	Gly	
1230					1235				1240						1245	
GGC	TAC	AGT	TGT	CGC	TGC	TTG	CCT	GGC	TTT	GCT	GGG	GAG	CGT	TGT	GAG	3792
Gly	Tyr	Ser	Cys	Arg	Cys	Leu	Pro	Gly	Phe	Ala	Gly	Glu	Arg	Cys	Glu	
				1250					1255					1260		
GGA	GAC	ATC	AAC	GAG	TGC	CTC	TCC	AAC	CCC	TGC	AGC	TCT	GAG	GGC	AGC	3840
Gly	Asp	Ile	Asn	Glu	Cys	Leu	Ser	Asn	Pro	Cys	Ser	Ser	Glu	Gly	Ser	
			1265					1270					1275			
CTG	GAC	TGT	ATA	CAG	CTC	ACC	AAT	GAC	TAC	CTG	TGT	GTT	TGC	CGT	AGT	3888
Leu	Asp	Cys	Ile	Gln	Leu	Thr	Asn	Asp	Tyr	Leu	Cys	Val	Cys	Arg	Ser	
	1280						1285					1290				
GCC	TTT	ACT	GGC	CGG	CAC	TGT	GAA	ACC	TTC	GTC	GAT	GTG	TGT	CCC	CAG	3936
Ala	Phe	Thr	Gly	Arg	His	Cys	Glu	Thr	Phe	Val	Asp	Val	Cys	Pro	Gln	
	1295					1300					1305					
ATG	CCC	TGC	CTG	AAT	GGA	GGG	ACT	TGT	GCT	GTG	GCC	AGT	AAC	ATG	CCT	3984
Met	Pro	Cys	Leu	Asn	Gly	Gly	Thr	Cys	Ala	Val	Ala	Ser	Asn	Met	Pro	
1310					1315					1320					1325	
GAT	GGT	TTC	ATT	TGC	CGT	TGT	CCC	CCG	GGA	TTT	TCC	GGG	GCA	AGG	TGC	4032
Asp	Gly	Phe	Ile	Cys	Arg	Cys	Pro	Pro	Gly	Phe	Ser	Gly	Ala	Arg	Cys	
				1330					1335					1340		
CAG	AGC	AGC	TGT	GGA	CAA	GTG	AAA	TGT	AGG	AAG	GGG	GAG	CAG	TGT	GTG	4080
Gln	Ser	Ser	Cys	Gly	Gln	Val	Lys	Cys	Arg	Lys	Gly	Glu	Gln	Cys	Val	
			1345					1350					1355			
CAC	ACC	GCC	TCT	GGA	CCC	CGC	TGC	TTC	TGC	CCC	AGT	CCC	CGG	GAC	TGC	4128
His	Thr	Ala	Ser	Gly	Pro	Arg	Cys	Phe	Cys	Pro	Ser	Pro	Arg	Asp	Cys	
		1360					1365					1370				
GAG	TCA	GGC	TGT	GCC	AGT	AGC	CCC	TGC	CAG	CAC	GGG	GGC	AGC	TGC	CAC	4176
Glu	Ser	Gly	Cys	Ala	Ser	Ser	Pro	Cys	Gln	His	Gly	Gly	Ser	Cys	His	
	1375					1380					1385					
CCT	CAG	CGC	CAG	CCT	CCT	TAT	TAC	TCC	TGC	CAG	TGT	GCC	CCA	CCA	TTC	4224
Pro	Gln	Arg	Gln	Pro	Pro	Tyr	Tyr	Ser	Cys	Gln	Cys	Ala	Pro	Pro	Phe	
1390					1395					1400					1405	
TCG	GGT	AGC	CGC	TGT	GAA	CTC	TAC	ACG	GCA	CCC	CCC	AGC	ACC	CCT	CCT	4272
Ser	Gly	Ser	Arg	Cys	Glu	Leu	Tyr	Thr	Ala	Pro	Pro	Ser	Thr	Pro	Pro	
				1410					1415					1420		
GCC	ACC	TGT	CTG	AGC	CAG	TAT	TGT	GCC	GAC	AAA	GCT	CGG	GAT	GGC	GTC	4320
Ala	Thr	Cys	Leu	Ser	Gln	Tyr	Cys	Ala	Asp	Lys	Ala	Arg	Asp	Gly	Val	
			1425					1430					1435			

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TGT Cys	GAT Asp	GAG Glu 1440	GCC Ala	TGC Cys	AAC Asn	AGC Ser	CAT His 1445	GCC Ala	TGC Cys	CAG Gln	TGG Trp	GAT Asp 1450	GGG Gly	GGT Gly	GAC Asp	4368
TGT Cys	TCT Ser 1455	CTC Leu	ACC Thr	ATG Met	GAG Glu	AAC Asn 1460	CCC Pro	TGG Trp	GCC Ala	AAC Asn 1465	TGC Cys	TCC Ser	TCC Ser	CCA Pro	CTT Leu	4416
CCC Pro 1470	TGC Cys	TGG Trp	GAT Asp	TAT Tyr	ATC Ile 1475	AAC Asn	AAC Asn	CAG Gln	TGT Cys	GAT Asp 1480	GAG Glu	CTG Leu	TGC Cys	AAC Asn	ACG Thr 1485	4464
GTC Val	GAG Glu	TGC Cys	CTG Leu	TTT Phe 1490	GAC Asp	AAC Asn	TTT Phe	GAA Glu	TGC Cys 1495	CAG Gln	GGG Gly	AAC Asn	AGC Ser	AAG Lys 1500	ACA Thr	4512
TGC Cys	AAG Lys	TAT Tyr	GAC Asp 1505	AAA Lys	TAC Tyr	TGT Cys	GCA Ala	GAC Asp 1510	CAC His	TTC Phe	AAA Lys	GAC Asp	AAC Asn 1515	CAC His	TGT Cys	4560
AAC Asn	CAG Gln 1520	GGG Gly	TGC Cys	AAC Asn	AGT Ser	GAG Glu	GAG Glu 1525	TGT Cys	GGT Gly	TGG Trp	GAT Asp	GGG Gly 1530	CTG Leu	GAC Asp	TGT Cys	4608
GCT Ala 1535	GCT Ala	GAC Asp	CAA Gln	CCT Pro	GAG Glu	AAC Asn 1540	CTG Leu	GCA Ala	GAA Glu	GGT Gly	ACC Thr 1545	CTG Leu	GTT Val	ATT Ile	GTG Val	4656
GTA Val 1550	TTG Leu	ATG Met	CCA Pro	CCT Pro	GAA Glu 1555	CAA Gln	CTG Leu	CTC Leu	CAG Gln	GAT Asp 1560	GCT Ala	CGC Arg	AGC Ser	TTC Phe	TTG Leu 1565	4704
CGG Arg	GCA Ala	CTG Leu	GGT Gly	ACC Thr 1570	CTG Leu	CTC Leu	CAC His	ACC Thr	AAC Asn 1575	CTG Leu	CGC Arg	ATT Ile	AAG Lys	CGG Arg 1580	GAC Asp	4752
TCC Ser	CAG Gln	GGG Gly	GAA Glu 1585	CTC Leu	ATG Met	GTG Val	TAC Tyr	CCC Pro 1590	TAT Tyr	TAT Tyr	GGT Gly	GAG Glu	AAG Lys 1595	TCA Ser	GCT Ala	4800
GCT Ala	ATG Met 1600	AAG Lys	AAA Lys	CAG Gln	AGG Arg	ATG Met	ACA Thr 1605	CGC Arg	AGA Arg	TCC Ser	CTT Leu	CCT Pro 1610	GGT Gly	GAA Glu	CAA Gln	4848
GAA Glu 1615	CAG Gln	GAG Glu	GTG Val	GCT Ala	GGC Gly	TCT Ser 1620	AAA Lys	GTC Val	TTT Phe	CTG Leu 1625	GAA Glu	ATT Ile	GAC Asp	AAC Asn	CGC Arg	4896
CAG Gln 1630	TGT Cys	GTT Val	CAA Gln	GAC Asp	TCA Ser 1635	GAC Asp	CAC His	TGC Cys	TTC Phe	AAG Lys 1640	AAC Asn	ACG Thr	GAT Asp	GCA Ala 1645	GCA Ala	4944
GCA Ala	GCT Ala	CTC Leu	CTG Leu	GCC Ala 1650	TCT Ser	CAC His	GCC Ala	ATA Ile	CAG Gln 1655	GGG Gly	ACC Thr	CTG Leu	TCA Ser	TAC Tyr 1660	CCT Pro	4992
CTT Leu	GTG Val	TCT Ser	GTC Val 1665	GTC Val	AGT Ser	GAA Glu	TCC Ser	CTG Leu 1670	ACT Thr	CCA Pro	GAA Glu	CGC Arg	ACT Thr 1675	CAG Gln	CTC Leu	5040
CTC Leu	TAT Tyr 1680	CTC Leu	CTT Leu	GCT Ala	GTT Val	GCT Ala	GTT Val 1685	GTC Val	ATC Ile	ATT Ile	CTG Leu	TTT Phe 1690	ATT Ile	ATT Ile	CTG Leu	5088
CTG Leu 1695	GGG Gly	GTA Val	ATC Ile	ATG Met	GCA Ala	AAA Lys 1700	CGA Arg	AAG Lys	CGT Arg	AAG Lys	CAT His 1705	GGC Gly	TCT Ser	CTC Leu	TGG Trp	5136

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CTG	CCT	GAA	GGT	TTC	ACT	CTT	CGC	CGA	GAT	GCA	AGC	AAT	CAC	AAG	CGT	5184
Leu	Pro	Glu	Gly	Phe	Thr	Leu	Arg	Arg	Asp	Ala	Ser	Asn	His	Lys	Arg	
1710					1715					1720					1725	
CGT	GAG	CCA	GTG	GGA	CAG	GAT	GCT	GTG	GGG	CTG	AAA	AAT	CTC	TCA	GTG	5232
Arg	Glu	Pro	Val	Gly	Gln	Asp	Ala	Val	Gly	Leu	Lys	Asn	Leu	Ser	Val	
				1730					1735					1740		
CAA	GTC	TCA	GAA	GCT	AAC	CTA	ATT	GGT	ACT	GGA	ACA	AGT	GAA	CAC	TGG	5280
Gln	Val	Ser	Glu	Ala	Asn	Leu	Ile	Gly	Thr	Gly	Thr	Ser	Glu	His	Trp	
			1745					1750					1755			
GTC	GAT	GAT	GAA	GGG	CCC	CAG	CCA	AAG	AAA	GTA	AAG	GCT	GAA	GAT	GAG	5328
Val	Asp	Asp	Glu	Gly	Pro	Gln	Pro	Lys	Lys	Val	Lys	Ala	Glu	Asp	Glu	
			1760				1765					1770				
GCC	TTA	CTC	TCA	GAA	GAA	GAT	GAC	CCC	ATT	GAT	CGA	CGG	CCA	TGG	ACA	5376
Ala	Leu	Leu	Ser	Glu	Glu	Asp	Asp	Pro	Ile	Asp	Arg	Arg	Pro	Trp	Thr	
	1775					1780					1785					
CAG	CAG	CAC	CTT	GAA	GCT	GCA	GAC	ATC	CGT	AGG	ACA	CCA	TCG	CTG	GCT	5424
Gln	Gln	His	Leu	Glu	Ala	Ala	Asp	Ile	Arg	Arg	Thr	Pro	Ser	Leu	Ala	
1790				1795					1800						1805	
CTC	ACC	CCT	CCT	CAG	GCA	GAG	CAG	GAG	GTG	GAT	GTG	TTA	GAT	GTG	AAT	5472
Leu	Thr	Pro	Pro	Gln	Ala	Glu	Gln	Glu	Val	Asp	Val	Leu	Asp	Val	Asn	
				1810					1815					1820		
GTC	CGT	GGC	CCA	GAT	GGC	TGC	ACC	CCA	TTG	ATG	TTG	GCT	TCT	CTC	CGA	5520
Val	Arg	Gly	Pro	Asp	Gly	Cys	Thr	Pro	Leu	Met	Leu	Ala	Ser	Leu	Arg	
			1825					1830				1835				
GGA	GGC	AGC	TCA	GAT	TTG	AGT	GAT	GAA	GAT	GAA	GAT	GCA	GAG	GAC	TCT	5568
Gly	Gly	Ser	Ser	Asp	Leu	Ser	Asp	Glu	Asp	Glu	Asp	Ala	Glu	Asp	Ser	
		1840					1845					1850				
TCT	GCT	AAC	ATC	ATC	ACA	GAC	TTG	GTC	TAC	CAG	GGT	GCC	AGC	CTC	CAG	5616
Ser	Ala	Asn	Ile	Ile	Thr	Asp	Leu	Val	Tyr	Gln	Gly	Ala	Ser	Leu	Gln	
	1855					1860				1865						
GCC	CAG	ACA	GAC	CGG	ACT	GGT	GAG	ATG	GCC	CTG	CAC	CTT	GCA	GCC	CGC	5664
Ala	Gln	Thr	Asp	Arg	Thr	Gly	Glu	Met	Ala	Leu	His	Leu	Ala	Ala	Arg	
1870					1875					1880					1885	
TAC	TCA	CGG	GCT	GAT	GCT	GCC	AAG	CGT	CTC	CTG	GAT	GCA	GGT	GCA	GAT	5712
Tyr	Ser	Arg	Ala	Asp	Ala	Ala	Lys	Arg	Leu	Leu	Asp	Ala	Gly	Ala	Asp	
				1890					1895					1900		
GCC	AAT	GCC	CAG	GAC	AAC	ATG	GGC	CGC	TGT	CCA	CTC	CAT	GCT	GCA	GTG	5760
Ala	Asn	Ala	Gln	Asp	Asn	Met	Gly	Arg	Cys	Pro	Leu	His	Ala	Ala	Val	
			1905					1910					1915			
GCA	GCT	GAT	GCC	CAA	GGT	GTC	TTC	CAG	ATT	CTG	ATT	CGC	AAC	CGA	GTA	5808
Ala	Ala	Asp	Ala	Gln	Gly	Val	Phe	Gln	Ile	Leu	Ile	Arg	Asn	Arg	Val	
			1920				1925					1930				
ACT	GAT	CTA	GAT	GCC	AGG	ATG	AAT	GAT	GGT	ACT	ACA	CCC	CTG	ATC	CTG	5856
Thr	Asp	Leu	Asp	Ala	Arg	Met	Asn	Asp	Gly	Thr	Thr	Pro	Leu	Ile	Leu	
	1935					1940						1945				
GCT	GCC	CGC	CTG	GCT	GTG	GAG	GGA	ATG	GTG	GCA	GAA	CTG	ATC	AAC	TGC	5904
Ala	Ala	Arg	Leu	Ala	Val	Glu	Gly	Met	Val	Ala	Glu	Leu	Ile	Asn	Cys	
1950					1955					1960					1965	
CAA	GCG	GAT	GTG	AAT	GCA	GTG	GAT	GAC	CAT	GGA	AAA	TCT	GCT	CTT	CAC	5952
Gln	Ala	Asp	Val	Asn	Ala	Val	Asp	Asp	His	Gly	Lys	Ser	Ala	Leu	His	
				1970					1975					1980		

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TGG	GCA	GCT	GCT	GTC	AAT	AAT	GTG	GAG	GCA	ACT	CTT	TTG	TTG	TTG	AAA	6000
Trp	Ala	Ala	Ala	Val	Asn	Asn	Val	Glu	Ala	Thr	Leu	Leu	Leu	Leu	Lys	
			1985					1990					1995			
AAT	GGG	GCC	AAC	CGA	GAC	ATG	CAG	GAC	AAC	AAG	GAA	GAG	ACA	CCT	CTG	6048
Asn	Gly	Ala	Asn	Arg	Asp	Met	Gln	Asp	Asn	Lys	Glu	Glu	Thr	Pro	Leu	
		2000					2005					2010				
TTT	CTT	GCT	GCC	CGG	GAG	GGG	AGC	TAT	GAA	GCA	GCC	AAG	ATC	CTG	TTA	6096
Phe	Leu	Ala	Ala	Arg	Glu	Gly	Ser	Tyr	Glu	Ala	Ala	Lys	Ile	Leu	Leu	
	2015					2020					2025					
GAC	CAT	TTT	GCC	AAT	CGA	GAC	ATC	ACA	GAC	CAT	ATG	GAT	CGT	CTT	CCC	6144
Asp	His	Phe	Ala	Asn	Arg	Asp	Ile	Thr	Asp	His	Met	Asp	Arg	Leu	Pro	
2030					2035					2040					2045	
CGG	GAT	GTG	GCT	CGG	GAT	CGC	ATG	CAC	CAT	GAC	ATT	GTG	CGC	CTT	CTG	6192
Arg	Asp	Val	Ala	Arg	Asp	Arg	Met	His	His	Asp	Ile	Val	Arg	Leu	Leu	
				2050					2055					2060		
GAT	GAA	TAC	AAT	GTG	ACC	CCA	AGC	CCT	CCA	GGC	ACC	GTG	TTG	ACT	TCT	6240
Asp	Glu	Tyr	Asn	Val	Thr	Pro	Ser	Pro	Pro	Gly	Thr	Val	Leu	Thr	Ser	
			2065					2070					2075			
GCT	CTC	TCA	CCT	GTC	ATC	TGT	GGG	CCC	AAC	AGA	TCT	TTC	CTC	AGC	CTG	6288
Ala	Leu	Ser	Pro	Val	Ile	Cys	Gly	Pro	Asn	Arg	Ser	Phe	Leu	Ser	Leu	
		2080					2085					2090				
AAG	CAC	ACC	CCA	ATG	GGC	AAG	AAG	TCT	AGA	CGG	CCC	AGT	GCC	AAG	AGT	6336
Lys	His	Thr	Pro	Met	Gly	Lys	Lys	Ser	Arg	Arg	Pro	Ser	Ala	Lys	Ser	
	2095					2100					2105					
ACC	ATG	CCT	ACT	AGC	CTC	CCT	AAC	CTT	GCC	AAG	GAG	GCA	AAG	GAT	GCC	6384
Thr	Met	Pro	Thr	Ser	Leu	Pro	Asn	Leu	Ala	Lys	Glu	Ala	Lys	Asp	Ala	
2110					2115				2120						2125	
AAG	GGT	AGT	AGG	AGG	AAG	AAG	TCT	CTG	AGT	GAG	AAG	GTC	CAA	CTG	TCT	6432
Lys	Gly	Ser	Arg	Arg	Lys	Lys	Ser	Leu	Ser	Glu	Lys	Val	Gln	Leu	Ser	
			2130				2135						2140			
GAG	AGT	TCA	GTA	ACT	TTA	TCC	CCT	GTT	GAT	TCC	CTA	GAA	TCT	CCT	CAC	6480
Glu	Ser	Ser	Val	Thr	Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	
			2145				2150						2155			
ACG	TAT	GTT	TCC	GAC	ACC	ACA	TCC	TCT	CCA	ATG	ATT	ACA	TCC	CCT	GGG	6528
Thr	Tyr	Val	Ser	Asp	Thr	Thr	Ser	Ser	Pro	Met	Ile	Thr	Ser	Pro	Gly	
		2160					2165					2170				
ATC	TTA	CAG	GCC	TCA	CCC	AAC	CCT	ATG	TTG	GCC	ACT	GCC	GCC	CCT	CCT	6576
Ile	Leu	Gln	Ala	Ser	Pro	Asn	Pro	Met	Leu	Ala	Thr	Ala	Ala	Pro	Pro	
	2175					2180					2185					
GCC	CCA	GTC	CAT	GCC	CAG	CAT	GCA	CTA	TCT	TTT	TCT	AAC	CTT	CAT	GAA	6624
Ala	Pro	Val	His	Ala	Gln	His	Ala	Leu	Ser	Phe	Ser	Asn	Leu	His	Glu	
2190					2195					2200					2205	
ATG	CAG	CCT	TTG	GCA	CAT	GGG	GCC	AGC	ACT	GTG	CTT	CCC	TCA	GTG	AGC	6672
Met	Gln	Pro	Leu	Ala	His	Gly	Ala	Ser	Thr	Val	Leu	Pro	Ser	Val	Ser	
			2210				2215							2220		
CAG	TTG	CTA	TCC	CAC	CAC	CAC	ATT	GTG	TCT	CCA	GGC	AGT	GGC	AGT	GCT	6720
Gln	Leu	Leu	Ser	His	His	His	Ile	Val	Ser	Pro	Gly	Ser	Gly	Ser	Ala	
			2225				2230						2235			
GGA	AGC	TTG	AGT	AGG	CTC	CAT	CCA	GTC	CCA	GTC	CCA	GCA	GAT	TGG	ATG	6768
Gly	Ser	Leu	Ser	Arg	Leu	His	Pro	Val	Pro	Val	Pro	Ala	Asp	Trp	Met	
		2240					2245					2250				

AAC CGC ATG GAG GTG AAT GAG ACC CAG TAC AAT GAG ATG TTT GGT ATG Asn Arg Met Glu Val Asn Glu Thr Gln Tyr Asn Glu Met Phe Gly Met 2255 2260 2265	6816
GTC CTG GCT CCA GCT GAG GGC ACC CAT CCT GGC ATA GCT CCC CAG AGC Val Leu Ala Pro Ala Glu Gly Thr His Pro Gly Ile Ala Pro Gln Ser 2270 2275 2280 2285	6864
AGG CCA CCT GAA GGG AAG CAC ATA ACC ACC CCT CGG GAG CCC TTG CCC Arg Pro Pro Glu Gly Lys His Ile Thr Thr Pro Arg Glu Pro Leu Pro 2290 2295 2300	6912
CCC ATT GTG ACT TTC CAG CTC ATC CCT AAA GGC AGT ATT GCC CAA CCA Pro Ile Val Thr Phe Gln Leu Ile Pro Lys Gly Ser Ile Ala Gln Pro 2305 2310 2315	6960
GCG GGG GCT CCC CAG CCT CAG TCC ACC TGC CCT CCA GCT GTT GCG GGC Ala Gly Ala Pro Gln Pro Gln Ser Thr Cys Pro Pro Ala Val Ala Gly 2320 2325 2330	7008
CCC CTG CCC ACC ATG TAC CAG ATT CCA GAA ATG GCC CGT TTG CCC AGT Pro Leu Pro Thr Met Tyr Gln Ile Pro Glu Met Ala Arg Leu Pro Ser 2335 2340 2345	7056
GTG GCT TTC CCC ACT GCC ATG ATG CCC CAG CAG GAC GGG CAG GTA GCT Val Ala Phe Pro Thr Ala Met Met Pro Gln Gln Asp Gly Gln Val Ala 2350 2355 2360 2365	7104
CAG ACC ATT CTC CCA GCC TAT CAT CCT TTC CCA GCC TCT GTG GGC AAG Gln Thr Ile Leu Pro Ala Tyr His Pro Phe Pro Ala Ser Val Gly Lys 2370 2375 2380	7152
TAC CCC ACA CCC CCT TCA CAG CAC AGT TAT GCT TCC TCA AAT GCT GCT Tyr Pro Thr Pro Pro Ser Gln His Ser Tyr Ala Ser Ser Asn Ala Ala 2385 2390 2395	7200
GAG CGA ACA CCC AGT CAC AGT GGT CAC CTC CAG GGT GAG CAT CCC TAC Glu Arg Thr Pro Ser His Ser Gly His Leu Gln Gly Glu His Pro Tyr 2400 2405 2410	7248
CTG ACA CCA TCC CCA GAG TCT CCT GAC CAG TGG TCA AGT TCA TCA CCC Leu Thr Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Ser Pro 2415 2420 2425	7296
CAC TCT GCT TCT GAC TGG TCA GAT GTG ACC ACC AGC CCT ACC CCT GGG His Ser Ala Ser Asp Trp Ser Asp Val Thr Thr Ser Pro Thr Pro Gly 2430 2435 2440 2445	7344
GGT GCT GGA GGA GGT CAG CGG GGA CCT GGG ACA CAC ATG TCT GAG CCA Gly Ala Gly Gly Gly Gln Arg Gly Pro Gly Thr His Met Ser Glu Pro 2450 2455 2460	7392
CCA CAC AAC AAC ATG CAG GTT TAT GCG TGAGAGAGTC CACCTCCAGT Pro His Asn Asn Met Gln Val Tyr Ala 2465 2470	7439
GTAGAGACAT AACTGACTTT TGTAATGCT GCTGAGGAAC AAATGAAGGT CATCCGGGAG	7499
AGAAATGAAG AAATCTCTGG AGCCAGCTTC TAGAGGTAGG AAAGAGAAGA TGTTCTTATT	7559
CAGATAATGC AAGAGAAGCA ATTCGTCAGT TTCACTGGGT ATCTGCAAGG CTTATTGATT	7619
ATTCTAATCT AATAAGACAA GTTTGTGGAA ATGCAAGATG AATACAAGCC TTGGGTCCAT	7679
GTTTACTCTC TTCTATTTGG AGAATAAGAT GGATGCTTAT TGAAGCCCAG ACATTCTTGC	7739
AGCTTGGACT GCATTTTAAG CCCTGCAGGC TTCTGCCATA TCCATGAGAA GATTCTACAC	7799

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TAGCGTCCTG	TTGGGAATTA	TGCCCTGGAA	TTCTGCCTGA	ATTGACCTAC	GCATCTCCTC	7859
CTCCTTGGAC	ATTCTTTTGT	CTTCATTTGG	TGCTTTTGGT	TTTGCACCTC	TCCGTGATTG	7919
TAGCCCTACC	AGCATGTTAT	AGGGCAAGAC	CTTTGTGCTT	TTGATCATTC	TGGCCCATGA	7979
AAGCAACTTT	GGTCTCCTTT	CCCCTCCTGT	CTTCCCGGTA	TCCCTTGGAG	TCTCACAAGG	8039
TTTACTTTGG	TATGGTTCTC	AGCACAAACC	TTTCAAGTAT	GTTGTTTCTT	TGGAAAATGG	8099
ACATACTGTA	TTGTGTTCTC	CTGCATATAT	CATTCCTGGA	GAGAGAAGGG	GAGAAGAATA	8159
CTTTTCTTCA	ACAAATTTTG	GGGGCAGGAG	ATCCCTTCAA	GAGGCTGCAC	CTTAATTTTT	8219
CTTGTCCTGT	TGCAGGTCTT	CATATAAACT	TTACCAGGAA	GAAGGGTGTG	AGTTTGTTGT	8279
TTTTCTGTGT	ATGGGCCTGG	TCAGTGTAAG	GTTTTATCCT	TGATAGTCTA	GTTACTATGA	8339
CCCTCCCCAC	TTTTTTAAAA	CCAGAAAAAG	GTTTGGAATG	TTGGAATGAC	CAAGAGACAA	8399
GTTAACTCGT	GCAAGAGCCA	GTTACCCACC	CACAGGTCCC	CCTACTTCCT	GCCAAGCATT	8459
CCATTGACTG	CCTGTATGGA	ACACATTTGT	CCCAGATCTG	AGCATTCTAG	GCCTGTTTCA	8519
CTCACTCACC	CAGCATATGA	AACTAGTCTT	AACTGTTGAG	CCTTTCCTTT	CATATCCACA	8579
GAAGACACTG	TCTCAAATGT	TGTACCCTTG	CCATTTAGGA	CTGAACCTTC	CTTAGCCCAA	8639
GGGACCCAGT	GACAGTTGTC	TTCCGTTTGT	CAGATGATCA	GTCTCTACTG	ATTATCTTGC	8699
TGCTTAAAGG	CCTGCTCACC	AATCTTTCTT	TCACACCGTG	TGGTCCGTGT	TACTGGTATA	8759
CCCAGTATGT	TCTCACTGAA	GACATGGACT	TTATATGTTC	AAGTGCAGGA	ATTGGAAAGT	8819
TGGACTTGTT	TTCTATGATC	CAAAACAGCC	CTATAAGAAG	GTTGGAAAAG	GAGGAACTAT	8879
ATAGCAGCCT	TTGCTATTTT	CTGCTACCAT	TTCTTTTCCT	CTGAAGCGGC	CATGACATTC	8939
CCTTTGGCAA	CTAACGTAGA	AACTCAACAG	AACATTTTCC	TTTCCTAGAG	TCACCTTTTA	8999
GATGATAATG	GACAACTATA	GACTTGCTCA	TTGTTCAGAC	TGATTGCCCC	TCACCTGAAT	9059
CCACTCTCTG	TATTCATGCT	CTTGGCAATT	TCTTTGACTT	TCTTTTAAGG	GCAGAAGCAT	9119
TTTAGTTAAT	TGTAGATAAA	GAATAGTTTT	CTTCCTCTTC	TCCTTGGGCC	AGTTAATAAT	9179
TGGTCCATGG	CTACACTGCA	ACTTCCGTCC	AGTGCTGTGA	TGCCCATGAC	ACCTGCAAAA	9239
TAAGTTCTGC	CTGGGCATTT	TGTAGATATT	AACAGGTGAA	TTCCCGACTC	TTTTGGTTTG	9299
AATGACAGTT	CTCATTCCTT	CTATGGCTGC	AAGTATGCAT	CAGTGCTTCC	CACTTACCTG	9359
ATTTGTCTGT	CGGTGGCCCC	ATATGGAAAC	CCTGCGTGTC	TGTTGGCATA	ATAGTTTACA	9419
AATGGTTTTT	TCAGTCCTAT	CCAAATTTAT	TGAACCAACA	AAAATAATTA	CTTCTGCCCT	9479
GAGATAAGCA	GATTAAGTTT	G TTCATTCTC	TGCTTTATTC	TCTCCATGTG	GCAACATTCT	9539
GTCAGCCTCT	TTCATAGTGT	GCAAACATTT	TATCATTCTA	AATGGTGACT	CTCTGCCCTT	9599
GGACCCATTT	ATTATTCACA	GATGGGGAGA	ACCTATCTGC	ATGGACCCTC	ACCATCCTCT	9659
GTGCAGCACA	CACAGTGCAG	GGAGCCAGTG	GCGATGGCGA	TGACTTTCTT	CCCCTGGGAA	9719
TTCC						9723